

OM protein - protein search, using sw model.			
Run on:	July 29, 2003, 09:50:12 ; Search time 23 Seconds (without alignments) 2119.892 Million cell updates/sec		
Title:	US-09-977-261-2		
Perfect score:	2671		
Sequence:	1 MAGRGLSVWRAGHGCDSAE..... PASVSGQDADGSTSPRSQEP 507		
Scoring table:	BLOSUM62		
Gapop:	10.0 , Gapext 0.5		
Searched:	283308 seqs, 96168682 residues		
Total number of hits satisfying chosen parameters:	283308		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries		
Database :	PIR 7.6:*		
	1: PIR1:*		
	2: PIR2:*		
	3: PIR3:*		
	4: PIR4:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	2671	100.0 507 2 A55625	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
2	2445	91.5 527 2 A49865	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
3	2341	87.6 505 2 159296	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
4	2221	83.2 467 2 156579	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
5	2209	82.7 465 2 148925	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
6	2153	46.9 450 2 141973	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
7	1245	46.6 450 1 JH0559	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
8	1242	46.5 450 1 S15094	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
9	1227	46.0 450 2 148929	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
10	762	45.5 507 1 A39939	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
11	751	45.5 509 1 148845	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
12	742	45.5 509 1 OHULK	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
13	736	27.6 545 2 S52313	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
14	735	27.5 533 1 TVCHS	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
15	734	27.5 526 1 TVFV60	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
16	734	27.5 568 1 TVFVSI	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
17	734	27.5 557 1 TVFVS2	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
18	733	27.5 546 2 S52314	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
19	731	27.4 587 1 TVFVPR	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
20	730	27.3 526 2 S20808	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
21	730	27.3 526 2 S26420	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
22	727	27.2 523 1 TVFVMT	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
23	724	27.1 526 1 OKFVYR	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
24	724	27.1 532 1 A34104	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
25	724	27.1 532 1 B34104	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
26	724	27.1 1520 1 TVFFA	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
27	723	27.1 527 1 TVFVR	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
28	720	27.1 505 1 TVHUHC	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
29	26.9	542 1 TVHUSC	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
ALIGNMENTS			
30	716.5	26.8 526 2 S15582	protein-tyrosine k
31	716	26.8 505 1 S24550	protein-tyrosine k
32	714	25.7 541 1 A43610	protein-tyrosine k
33	713	26.7 506 1 S24553	protein-tyrosine k
34	713	26.7 512 1 156160	protein-tyrosine k
35	710	26.7 528 1 TVFVG9	protein-tyrosine k
36	710	26.6 541 2 S31645	protein-tyrosine k
37	710	26.6 543 1 TVHUY5	protein-tyrosine k
38	709	26.5 537 2 151592	protein-tyrosine k
39	707	26.5 512 1 TVHULY	protein-tyrosine k
40	706	26.4 541 1 TVCHYS	protein-tyrosine k
41	706	26.4 542 1 A49114	protein-tyrosine k
42	705	26.4 544 2 151593	protein-tyrosine k
43	701	26.2 512 1 A39719	protein-tyrosine k
44	700.5	26.2 503 1 J01321	protein-tyrosine k
45	699.5	26.2 536 2 S33569	protein-tyrosine k

A; Residues: 41-505 <AVR>
 R; Kaneko, Y.; Nonoguchi, K.; Fukuyama, H.; Takano, S.; Higashitsuji, H.; Nishiyama, H.;
 Onogeno, 10, 945-952, 1995
 A; Title: Presence of alternative 5' untranslated sequences and identification of cells expressing
 A; Reference number: 149621; MOID:95206787; PMID:7898936
 A; Status: translated from GB/EMBL/DDJB
 A; Molecule type: mRNA
 A; Residues: 41-505 <RE3>
 A; Cross-references: GB:D45243; NID:9639858; PIDN:BA00199.1; PID:9639859
 C; Genetics:
 A; Gene: Nck; P56ntk
 A; Introns: 23/3
 C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F; 51-103-/Domain: SH3 homology <SH3>
 F; 120-209-/Domain: SH2 homology <SH2>
 F; 231-483-/Domain: protein kinase homology <KIN>
 F; 239-247-/Region: protein kinase ATP-binding motif
 Query Match 87.6%; Score 2341; DB 2; Length 505;
 Best Local Similarity 87.4%; Pred. No. 3.7e-113; Mismatches 443; Conservative 27; Mismatches 35; Indels 2; Gaps 2;
 Matches 1
 1 MAGRSILYSMRAFGCGDSAEELPRVSPRFRAWHPPVPSARMPTTRWAPTCITKCEH 60
 Db 1 MARRSRSVSLWLFEGWS-RDLPVPRFAGWHPAARMP-T-RWAGTQCMWCKENS 58
 QY 61 RPKPGELAFRKGDVVTTLEAGENSKSYRKHTSGQEGGLAAGALREREAISADPKLSM 120
 Db 59 RPKPGELAFRKGDVVTTLEAGENSKSYRKHTSGQEGGLAAGALREREAISADPKLSM 118
 QY 121 PWFHGKTSGOPAVQQLQPPEPDGLFLVRESARHPGDYLVLCYSFGRDVTHYRLHRDGHLT 180
 Db 119 PWFHGKTSGQEAIQQLQPPEDGLFLVRESARHPGDYLVLCYSFGRDVTHYRLHRDGHLT 178
 QY 181 DEAVFCNLMDMVYEVNSKDKGAICTKLVRKRHKDTKSASEELAGWLNQHQHTLGQ 240
 Db 179 DEAFCFCNLMDMVYEVNSKDKGAICTKLVRKRHKDTKSASEELAGWLNQHQHTLGQ 238
 QY 241 IGEGERGAVALOGEYLGQKAVAKNIKDVTQAFDTEAVMTKMOHENLVLGLVHLQG 300
 Db 239 IGEGERGAVALOGEYLGQKAVAKNIKDVTQAFDTEAVMTKLOQNLRLVRLGLVHLQG 298
 QY 301 YIVMEVNSKGNLNFRTGRALVNIAQLQFLSLVAEGMELYLESKKVLRHDLAARNTLV 360
 Db 299 YIVMEVNSKGNLNFRTGRALVNIAQLQFLALHVAEGMELYLESKKVLRHDLAARNTLV 358
 QY 361 SEDLVAKVSDGLAKERKGIDSSRLPUKVMTAPEALKHGKPTSKSDYWSGCVLNUVEFSY 420
 Db 359 SEDLVAKVSDGLAKERKGIDSSRLPUKVMTAPEALKHGKPTSKSDYWSGCVLNUVEFSY 418
 QY 421 GRAPYPKMSLKEVSEAVEKGYRMEEPDGCPGSVHTLNGSCWEAEPARRPFRKIVEKLG 480
 Db 419 GRAPYPKMSLKEVSEAVEKGYRMEEPDGCPGSVHTLNGSCWEAEPARRPFRKIVEKLG 478
 QY 481 EIRSAGAPASVSGQDADGSTSPRSQP 507
 Db 479 EIRSAGAPASVSGQDADGSTSPRSQP 505

RESULT 4
 156579 protein-tyrosine kinase (EC 2.7.1.112) batk - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Mar-2000
 C;Accession: 156579
 C;Title: Identification and characterization of Batk, a predominantly brain-specific non-muscle protein kinase
 A;Reference number: 156579; MUID:95106341; PMID:7807586
 A;Status: preliminary; translated from GB/EMBL/DDJB
 Query Match 82.7%; Score 2209.5; DB 2; Length 465;

RESULT 5
 148926 protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
 N;Alternate names: csk-type protein-tyrosine kinase
 C;Species: Mus musculus (house mouse)
 C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 04-Feb-2000
 C;Accession: 148926
 R;Klages, S.; Adam, D.; Class, K.; Faronoli, J.; Bolen, J.B.; Penhallow, R.C.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994
 A;Title: Ctk: a protein tyrosine kinase related to Csk that defines an enzyme family.
 A;Reference number: A53469; MOID:9195789; PMID:7511815
 A;Accession: 148926
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-465 <RES>
 A;Cross-references: EMBL:U05210; NID:9450232; PIDN:AAA18829.1; PID:9450233
 C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 C;Accession: 13-63-/Domain: SH3 homology <SH3>
 F; 13-63-/Domain: SH2 homology <SH2>
 F; 80-169-/Domain: SH2 homology <SH2>
 F; 191-443-/Domain: protein kinase homology <KIN>
 F; 192-445-/Domain: protein kinase homology <KIN>
 F; 200-208-/Region: protein kinase ATP-binding motif
 Query Match 83.2%; Score 2221.5; DB 2; Length 467;
 Best Local Similarity 89.3%; Pred. No. 4.5e-107; Mismatches 417; Conservative 27; Mismatches 1; Indels 1; Gaps 1;
 Matches 1
 1 MPTRRWAPGTCITCCEHTTRPKGELAFRKGDVVTTLEAGENSKSYRKHTSGOBGLA 101
 Db 1 MPTRRWAPGTCITCCEHTTRPKGELAFRKGDVVTTLEAGENSKSYRKHTSGOBGLA 60
 QY 102 AGALRREALSADPKLSLMPFMFHGKTSQGQA1QQLQPPEDGLFLVRESARHPGDYLVCV 161
 Db 121 FGDRDVHYRLHDHSITIDEAVFCNLMDMVYEVNSKDKGAICTKLVRKRHKHTGSA 221
 Db 61 AAALRQEALSTDPKLSLMPFMFHGKTSQGQA1QQLQPPEDGLFLVRESARHPGDYLVCV 120
 QY 162 FGDRDVHYRLHDHSITIDEAVFCNLMDMVYEVNSKDKGAICTKLVRKRHKHTGSA 221
 Db 121 FGDRDVHYRLHDHSITIDEAVFCNLMDMVYEVNSKDKGAICTKLVRKRHKHTGSA 180
 QY 222 ELARAGWLLNQHHTLGQAOITGEGERGAVALOGEYLGQKAVAKNIKDVTQAFDDETAVMT 281
 Db 181 BLAKAWLIDLQHHTLGQAOITGEGERGAVALOGEYLGQKAVAKNIKDVTQAFDDETAVMT 240
 QY 282 KMQHENEVRLGLVHLQHGLYVMEVSKGNLNFRTGRALVNIAQLQFLSLVAEGM 341
 Db 301 YLESKLVVRLHDLAARNTLVLSLVDLAKRGLDSSRLPVKNTAPEALKNGR 360
 QY 401 FTSKSDWWSFGVLLNEVFSTGRAPPKMSLKEVSEAVEKGYRMEEPDGCPGVHMLSSC 460
 Db 361 FSSKSDWWSFGVLLNEVFSTGRAPPKMSLKEVSEAVEKGYRMEEPDGCPGVHMLSSC 420
 QY 461 WEAEPARRPFRKLAERLRSAGAPASVSGQDADGSTSPRSQP 507
 Db 421 WEAEPARRPFRKLAERLRSAGAPASVSGQDADGSTSPRSQP 467
 Query Match 82.7%; Score 2209.5; DB 2; Length 465;

Best Local Similarity	89.5%	Pred.	No.	1..9e-105;	Db	127 EHVRILISSSKLISIDEEVYFENLMQLVHRYTTADGLCSRLLPKWMEGTVAQDEFRSRS
Matches	417;	Conservative	23;	Mismatches	25;	Indels
					1;	Gaps
					1;	
Qy	42 MPTRRWAPOTQCITKCEHPRKGELARKRGDVITLEACENNSWYRKHTSGQEGILLA	Oy	227 GWILNLNQHUTLGQOIGECEFGAVLQGEYLQVAKWNKTCDTAQAFIDETAVMTKHOE			
Db	1 MPT-RWAQCTQCMKCEUSPKGELARKRGDVITLEACENNSWYRKHTSGQEGILLA	Db	187 GWAHLNMKDLKLQIQTGKDFGDMGQDGRNKVAVKCITNDATAQAFLAESAWMTQLRHS			
Qy	102 AGALREREAALISADPKLSLMPWFKISGOEAQOLQPEDGLFLVRESARHPGDYVLCWS	Oy	287 NLVRLGILHQ -GLIT-VMEHVSCKGNLYNLFTRGRALVNTPQLOFLSLHVAEGMEYLE			
Db	60 AAALRHRGEALSTDPKLSLMPWFKISGOEAQOLQPEDGLFLVRESARHPGDYVLCWS	Db	247 NLVQLLGIVVEERKSLYTPEYNAKGSLVDLRSRGSVLGGDCLLKPSLDVCEAMYLE			
Qy	162 FGDRVTHYVLRHGRGHTDEAFCCNLMDMVEHYTKDGAICTKLVRKRKGITKSAEE	Oy	345 SKVLUVRDIAARNLTVSDELVAKVSDGLAKAERKGKDSSRLPVKWTAPEALKHGKF			
Db	120 FGDRVTHYVLRHGRGHTDEAFCCNLMDMVEHYTKDGAICTKLVRKRKGITKSAEE	Db	307 ANNFVRHDLARNLNUSEDNTIAKVSDCLTKEASSTDGTGKLPVKWTAPEALKHGKFSTK			
Qy	222 ELARAGWLNLQHLTGAGIGEGERFGAVVQGEYLQVAKWNKTCDTAQAFIDETAVMT	Oy	405 SDWWSFGYLWIEFSYSGRAPHYPMKSLKEVSEAEVKYRMERPEPGCPSRVHLMSSWEAE			
Db	180 ELARAGWLNLQHLTGAGIGEGERFGAVVQGEYLQVAKWNKTCDTAQAFIDETAVMT	Db	367 SDWWSFGILLWEIYFSGRVPYPIPLKDVPRVEGYKMDPPDGCPAIVYEVEMKKWTLD			
Qy	282 KMOHENLYRLGVILVHQGXIVMEHVSCKGNLVNLVFLRTGRALVNTAQLOFLSLHVAEGME	Oy	465 PARRPFPKLAEKRELRSAGAPASSVGODGSNSPRSOEP			
Db	240 KLGHRNLVYLVLGVTIHGQLYIVMEHVSCKGNLVNLVFLRTGRALVNTAQLOFLSLHVAEGME	Db	427 PGHRPSFHOLREQL			
Qy	342 YLESKKLVRDIAARNLTVSDELVAKVSDGLAKAERKGKDSSRLPVKWTAPEALKHGKF	RESULT 6	JH0559			
Db	300 YLESKKLVRDIAARNLTVSDELVAKVSDGLAKAERKGKDSSRLPVKWTAPEALKHGKF	protein-tyrosine kinase (EC 2.7.1.112) CSK - human				
Qy	402 TSKDWVSWGIVLWEVFSYSGRAPHYPMKSLKEVSEAEVKYRMERPEPGCPSRVHLMSSCW	Nt; Alternate names: protein-tyrosine kinase cyl; protein-tyrosine kinase T2				
Db	360 SSXSDWVSWGIVLWEVFSYSGRAPHYPMKSLKEVSEAEVKYRMERPEPGCPSRVHLMSSCW	C; Species: Homo sapiens (man)				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	C; Accession: JH0559				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	C; Date: 30-Jun-1992 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	R; Braeuninger, A.; Holtrich, U.; Strebhardt, K.; Ruebsamen-Waigmann, H.				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	Gene 110, 205-211, 1992				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Title: Isolation and characterization of a human gene that encodes a new subclass of protein-tyrosine kinases				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Reference number: S38818; MUID:93241739; PMID:7683131				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Reference number: JH0559; MUID:92156060; PMID:1371489				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Status: preliminary				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Molecule type: DNA				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Residues: 1..450 <SAB>				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Cross-references: EMBL:X59932; NID:930255; PIDN:CAA42556.1; PID:930256				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Experimental source: Lung				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	R; Braeuninger, A.; Kurn, T.; Strebhardt, K.; Ruebsamen-Waigmann, H.				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	Oncogene 8, 1365-1369, 1993				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Title: Characterization of the human CSK locus				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Reference number: S38818; MUID:93241739; PMID:7683131				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Reference number: S38818; MUID:92156060; PMID:1371489				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Status: preliminary				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Molecule type: mRNA				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Residues: 1..450 				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Cross-references: EMBL:X74765; NID:9402582; PIDN:CAB59562.1; PID:96077093				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	R; Partanen, J.; Armstrong, E.; Bergman, M.; Maekelae, T.P.; Hirvonen, H.; Huebner, K.				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	Oncogene 6, 2013-2018, 1991				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Title: c-f1 encodes a putative cytoplasmic tyrosine kinase lacking the conserved tyrosine residue at position 1450				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Reference number: S19024; MUID:92050797; PMID:1945408				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Status: preliminary				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Molecule type: mRNA				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Residues: 1..450 <PAR>				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Cross-references: EMBL:X60114; NID:930314; PIDN:CAA42713.1; PID:930315				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	R; Holtrich, U.; Braeuninger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	Proc. Natl. Acad. Sci. U.S.A., 88, 10411-10415, 1991				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member of the CSK family				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Reference number: S19025; MUID:92073297; PMID:1720539				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Status: preliminary; nucleic acid sequence not shown				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Residues: 1..450 <HOL>				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Cross-references: EMBL:X59932; NID:930255; PIDN:CAA42556.1; PID:930256				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Note: this sequence was submitted to the EMBL Data Library, June 1991				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	C; Comment: This protein lacks the N-myristylation and autophosphorylation sites present				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	C; Genetics:				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Gene: GDB:CSK				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Cross-references: GDB:131642; OMIM:124095				
Db	420 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Map position: 15q23-15q25				
Qy	462 EAEPARRPPPFKLAEKRELRSAGAPASSVGODGSNSPRSOEP	A; Introns: 5/3; 43/3; 81/2; 154/3; 186/1; 208/1; 241/2; 271/3; 296/2; 361/3; 390/3				

C; Function:

A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F; 16-65/Domain: SH3 homology <SH3>

F; 82-171/Domain: SH2 homology <SH2>

F; 193-447/Domain: protein kinase homology <KIN>

F; 201-209/Region: protein kinase ATP-binding motif

F; 222/Active site: Lys #status predicted

Query Match 46.5%; Score 1245.5; DB 1; Length 450;

Best Local Similarity 54.1%; Pred. No. 4.6e-57; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTOCTKCEHTRPKPGELAFRKGDWVTLACENKSMYRVIKHTSGOEGLLAGALR 106

Db 8 WPSGTECIAKYNFHGTAEQDLPCKDVLTVAVTKDPNPKAKNV-GREGIIPANYQ 66

Qy 107 EREALSADPKLISLMPWFHKTSQGQBAVQQLQPPEGLYRESARHPGCVLCSFGRDV 166

Db 67 KREGVKAGTKLISLMPWFHKTRDGAERLRLYPPEGLYRESTNPGDYTLCSGDKV 126

Qy 167 IHYRVIHRDGHLTIDEAVFFCNLMQDVHEYSKDKGAICTKLRVRPRKHGTSAEFLARA 226

Db 127 EHRYIMHASKLSIDEDEVYFNLMQLEVHHTSDAGLICTRLIKPKVMESIVAAQDEFYRS 186

Qy 227 GWLLNLQHLTGQAOGEGERGAVLGEYLGQKVAKNIKDVTAAFLDTAVWTKMQUE 286

Db 187 GWALNNKELKLQLQTIGKGEFDVMDYRGNKAVCKINDATACFLAEASVMTQLRHS 246

Qy 287 NLVRLLGVILHQ-GLYTVMERHSKGNLVNLFRTRGRALNTAQIQLFSIHVAEEMYLE 344

Db 247 NLVOLQGVIVTEKKGLSVLDRSRGSVLLGDCLIKESDUDCEAMEYLE 306

Qy 345 SKKLVIRDLAARNLIVSEDLYAKVSDFGLAKAERKGDDSSRLPVWTAPEALKHCKFTSK 404

Db 307 GNNFVHRLDAARNLIVSEDLYAKVSDFGLAKAERKGDDSSRLPVWTAPEALKHCKFTSK 366

Qy 405 SDWWSRGVLIWEVFSYGRAPYKPKMSLKEVSEAVKGRYMRPMEPPGCPGPVHL MSSWEAE 464

Db 367 SDWWSFGILLMEIYSFGRVYPYPRFLKDWPVPRVERGKYKMDAPDGCPPAVYEMVNKNWHLID 426

Qy 465 PARRPFKRKLAEKL 478

Db 427 AAMRPSFLQREQL 440

RESULT 8

S15094 protein-tyrosine kinase (EC 2.7.1.112) CSK - rat

N; Alternate names: c-src kinase; tyro-13 kinase

C; Species: Rattus norvegicus (Norway rat)

C; Date: 30-Jun-1993 #sequence_change 30-Jun-1993 #text_change 11-Jun-1999

C; Accession: S15094; S8500; PT0195

R; Niida, S.; Obara, M.; MacAuley, A.; Cooper, J.A.; Nakagawa, H.

Nature 351, 659-72, 1991

A; Title: Cloning of a complementary DNA for a protein-tyrosine kinase that specifically

A; Reference number: S15094; MUID:91226538; PMID:1709258

A; Accession: S15094

A; Molecule type: mRNA

A; Residues: 1-450 <NAD1>

A; Cross-references: EMBL:X58631; NID:957507; PIDN:CAA41484.1; PID:957508

A; Accession: S18500

A; Molecule type: protein

A; Residues: 44-49; 54-67; 77-86; 126-137; 330-337; 352-360; 367-376; 394-401 <NAD>

R; Lai, C.; Lemke, G.

Neuron 6, 691-704, 1991

A; Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A; Reference number: PT0183; MUID:9122560; PMID:2025425

A; Molecule type: mRNA

A; Experimental source: sciatic nerve

C; Genetics:

A; Gene: tyro-13

C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase

F; 16-65/Domain: SH3 homology <SH3>

F; 82-171/Domain: SH2 homology <SH2>

F; 193-447/Domain: protein kinase homology <KIN>

F; 201-209/Region: protein kinase ATP-binding motif

F; 222/Active site: Lys #status predicted

Query Match 46.5%; Score 1242.5; DB 1; Length 450;

Best Local Similarity 54.1%; Pred. No. 6.6e-57; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTOCTKCEHTRPKPGELAFRKGDWVTLACENKSMYRVIKHTSGOEGLLAGALR 106

Db 8 WPSGTECIAKYNFHGTAEQDLPCKDVLTVAVTKDPNPKAKNV-GREGIIPANYQ 66

Qy 107 EREALSADPKLISLMPWFHKTSQGQBAVQQLQPPEGLYRESARHPGCVLCSFGRDV 166

Db 67 KREGVKAGTKLISLMPWFHKTRDGAERLRLYPPEGLYRESTNPGDYTLCSGDKV 126

Qy 167 IHYRVIHRDGHLTIDEAVFFCNLMQDVHEYSKDKGAICTKLRVRPRKHGTSAEFLARA 226

Db 127 EHRYIMHASKLSIDEDEVYFNLMQLEVHHTSDAGLICTRLIKPKVMESIVAAQDEFYRS 186

Qy 227 GWLLNLQHLTGQAOGEGERGAVLGEYLGQKVAKNIKDVTAAFLDTAVWTKMQUE 286

Db 187 GWALNNKELKLQLQTIGKGEFDVMDYRGNKAVCKINDATACFLAEASVMTQLRHS 246

Qy 287 NLVRLLGVILHQ-GLYTVMERHSKGNLVNLFRTRGRALNTAQIQLFSIHVAEEMYLE 344

Db 247 NLVOLQGVIVTEKKGLSVLDRSRGSVLLGDCLIKESDUDCEAMEYLE 306

Qy 345 SKKLVIRDLAARNLIVSEDLYAKVSDFGLAKAERKGDDSSRLPVWTAPEALKHCKFTSK 404

Db 307 GNNFVHRLDAARNLIVSEDLYAKVSDFGLAKAERKGDDSSRLPVWTAPEALKHCKFTSK 366

Qy 405 SDWWSRGVLIWEVFSYGRAPYKPKMSLKEVSEAVKGRYMRPMEPPGCPGPVHL MSSWEAE 464

Db 367 SDWWSFGILLMEIYSFGRVYPYPRFLKDWPVPRVERGKYKMDAPDGCPPAVYEMVNKNWHLID 426

Qy 465 PARRPFKRKLAEKL 478

Db 427 AAMRPSFLQREQL 440

RESULT 9

I48929 protein-tyrosine kinase (EC 2.7.1.112) Csk - mouse

N; Alternate names: protein-tyrosine kinase Mpk-2

C; Species: Mus musculus (house mouse)

C; Date: 15-Mar-1995 #sequence_revision 15-Mar-1996 #text_change 18-Feb-2000

C; Accession: I48929; S30949

R; Klages, S.; Adam, D.; Class, K.; Farnoli, J.; Bolen, J.B.; Penhallow, R.C.

Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994

A; Title: Ctk: a protein tyrosine kinase related to Csk that defines an enzyme family.

A; Reference number: A53469; MUID:9419589; PMID:7511815

A; Accession: I48929

A; Molecule type: mRNA

A; Residues: 1-450 <RES>

A; Cross-references: EMBL:U05247; NID:9452471; PIDN:AAA18765.1; PID:9452472

A; Accession: PT0195

A; Molecule type: mRNA

A; Residues: 319-367 <LAI>

Neuron 6, 691-704, 1991

A; Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A; Reference number: PT0183; MUID:9122560; PMID:2025425

A; Molecule type: mRNA

A; Experimental source: sciatic nerve

Db 78 GDLGFERKGQQLRILE---QSGEWKKAQSLTTGQEGFIPFFWVAKANLSEE-----PWF 129
 QY 125 GKTSGQEAQVQOLOPPED---GLFLVRESAHRHPGDYVLCV----SFGRDWTHYRLHRG-G 176
 Db 130 KNLSSRKDAERKQLLAGPNTGGSFLIRESESTAGSFSLSVDFDQNQGEVVKHYKIRNLNG 189
 QY 177 HLTIDEAVFCNLMDMVEHYSKDKGAICTKLVRKRKHGTSAEELARRAGWLNLQHIT 236
 Db 190 GFYIISPRITPGLHLVRLVYNAASDGCLCTRLSPCQ---TOKPOKPWNHDEWEVPREPLK 246
 QY 237 LGAQIGEGERGAVIQLQGEYQGO-KVAVKNK-CDVTAQAFLETAVMTKHQHENIVRLIGV 294
 Db 247 LVERIGAGCQFGEVNGYYVNGHTKAVSKQGSMSPAFLAEANLMKQHQHQLVRLIYAV 306
 QY 295 ILHQGLYTMEHVSKGNLNUFLRTRGRALVNTAOOLLOFLSHVARGMEVYESKKLVHROIA 354
 Db 307 VTQEPPIVITTEYIMENGSLVDFLKTPSGIKLTINKLDDMAQIAEGMAFEERNYIHDRL 366
 QY 355 ARNLTILVSELDLVAKYSDFGJAKA---ERKGDSLRSRPLVWTAPALEKHKFTSKDSWVF 410
 Db 367 RANILVSDALSLCKRADFLGARLIDNEQEYAREGAKFPKTPAPEAINYGTFTIKSDWNSF 426
 Qy 411 GVLLMEVFPYGRAPKPKMILKEVSEAVEGYRMPPGPGPVAVLMSSCWEARPARPP 470
 Db 427 GILLTEIVFHGRIPPGMNTPEVTONLERGYRMVPRPDNCPPEELVQMLRUCWERPEDRPT 486
 QY 471 FRKLAEKL 478
 Db 487 FDYLRSVL 494

RESULT 13

S5313 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C;Species: Rous sarcoma virus
 C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Mar-2000
 C;Accession: S52313
 R;ratsoyan, A.; Yatsula, B.; Shtrutman, M.; Moihova, E.; Kaverina, I.; Musatkina, E.; Les submitted to the EMBL Data Library, January 1995
 A;Description: Two new isoforms of v-src oncogene isolated from low and high metastatic A;Accession number: S52313
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-545 <TAT>
 A;Cross-references: EMBL:X84074; NID:9663003; PIDN:CAA58891.1; PID:96630084
 C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 homology; SH3 R
 C;Keywords: Rtp; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F;108-157//Domain: SH3 homology <SH3>
 F;168-265//Domain: SH2 homology <SH2>
 F;285-543//Domain: protein kinase homology <KIN>
 F;293-301//Region: protein kinase Atp-binding motif
 F;2//Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;315//Active site: Lys #status predicted
 F;356//Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 Query Match Score 7.6%; DB 2; Length 555;
 Best Local Similarity 35.6%; Pred. No. 7.3e-31;
 Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16;

QY 14 HGCDSAEEPR----VSPLERLAWHPP-----PSARMTRRMAPGT-----51
 Db 26 HGGEPASOPPNKTLAPLAAAPRSSR--RPPASOHRRAADDTTHPSPSF--GTVANEPEKF 81
 QY 52 -----QCTTKCEMPRKIG-----ELAFRKGVVTLTEACENKSNWR 88
 Db 82 GDFWISDVTSPQARTLQAGVTFVALYDYESWIEITDJSFKGERQIVNTEG 140
 QY 89 VKHTSQGQQLAAGALRREALSDAPKLSIMMMPHGKSGQARVQOLOPPED---GLFLV 146
 Db 141 AHSVTGQGYGIPSNYVAPSDSIQE-----EWYFGKTRBESGRLLNPENPRTFLV 194
 QY 147 RESARHPGQWVICS----FGDVIHVFLHGD-HLTIDEAVFCNLMDMVEHYSKDK 200

RESULT 14

TVCHS protein-tyrosine kinase (EC 2.7.1.112) src - chicken
 N;Alternate names: kinase-related transforming protein src
 C;Species: Gallus gallus (chicken)
 C;Accession: A00630; 150217; A41256; C35650; A32432
 C;Accession: A00630; 150217; A41256; C35650; A32432
 R;Takeya, T.; Hanafusa, H.
 Cell 32, 881-890, 1983
 A;Title: Structure and sequence of the cellular gene homologous to the RSV src gene a
 A;Reference number: A00630; #sequence_revision 07-Oct-1994 #text_change 21-Jul-2000
 A;Accession: A00630
 A;Molecule type: DNA
 A;Residues: 1-500; R' 502-533 <TAK>
 A;Cross-references: GB:J00844; NID:9212700
 R;Takeya, T.; Hanafusa, H.
 Cell 34, 319, 1983
 A;Reference number: A90838
 A;Contents: annotation; erratum; correct translation of residue 526
 R;Takeya, T.; Hanafusa, H.
 J. Virol. 44, 12-18, 1982
 A;Title: DNA sequence of the viral and cellular src gene of chickens: II comparison o
 A;Reference number: I50217; MUID:83059861; PMID:6292480
 A;Accession: I50217
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 17 <TR>
 A;Cross-references: GB:J00808; NID:g211690; PIDN:AAA4873.1; PID:9211691
 A;Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr
 R;boraI, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
 Mol. Cell. Biol. 11, 4165-176, 1991
 A;Title: Analysis of cDNAs for the proto-oncogene c-src: heterogeneity in 5' exons and
 A;Reference number: A41256; MUID:91304409; PMID:1712905
 A;Accession: A41256
 A;Molecule type: mRNA
 A;Residues: 484-533 <DOR1>
 A;Cross references: GB:S43579; NID:9167994; PIDN:AB19353.1; PID:9233061
 A;Note: the authors translated the codon CAG for residue 527 as Glu
 R;Durai, T.; Wang, L.H.
 Mol. Cell. Biol. 10, 4068-4079, 1990
 A;Title: An alternative non-tyrosine protein kinase product of the c-src gene in chick
 A;Reference number: A35650; MUID:90318371; PMID:215117
 A;Accession: C35650
 A;Molecule type: mRNA
 A;Residues: 1-182, 'DPCIPLPSCIC' <DOR2>
 A;Cross references: GB:J57290; NID:9212703; PIDN:AA49078.1; PID:9212706
 A;Note: alternatively spliced mRNA exclusively replaces the long-form in skeletal mus
 A;Note: this ORF appears not to be translated
 R;Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.

Cell 57, 763-774, 1989
A;Title: Purified maturation promoting factor phosphorylates pp60(c-src) at the sites pht
A;Reference number: A32432; MUID:89249341; PMID:2470512
A;Accession: A32432
A;Molecule type: protein
A;Residues: 2-88 <SHE>
A;Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
C;Genetics:
A;Gene: src
C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein
F;18-137/Domain: SH2 homology <SH2>
F;18-245/Domain: SH2 homology <SH2>
F;205-523/Domain: protein kinase homology ATP-binding motif
F;273-281/Region: protein kinase homology <KIN>
F;273-281/Region: protein kinase homology <KIN>
F;273-281/Region: protein kinase homology <KIN>
F;12-48/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;12-48/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;31-46/Binding site: phosphate (Thr) (covalent) #status experimental
F;72/Binding site: phosphate (Ser) (covalent) #status predicted
F;72/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
F;416,521/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
Query Match 27.5%; Score 735; DB 1; Length 533;
Best Local Similarity 37.9%; Pred. No. 8e-31;
Matches 173; Conservative 76; Mismatches 162; Indels 42; Gaps 11;
Qy 6 ELAFRKGDVVTILEACENKSWKYRKHTSGOGLLAAGALREREALSADPKLSLMPWFHG 125
Db 9 DLSEKKERLQLQVNTEG-NWMLAISLTGTTGTYPSNVYAPSDSQAE-----EWFG 151
Qy 126 KISGQRAVQQLQPPED-GFLVRESARHGPDDYVLCV-----FGRDVIVHYRVLHD-GH 177
Db 152 KITRRESERLLNPNPGRPLFLVRESETTKGAYCLSVSDFDNAKLGVHKYKIRLDGG 211
Qy 178 LTIDEAVFCNLMDAYEHYSKDGAICTKL--VRRRKHGKSAEELARAGWLNLQHL 235
Db 212 FYITSRTQFSQIQLQVAYSKHADGLCHRLINVCPTSKPQPOQ---LAKDAWEIPRESL 267
Qy 236 TIGAIGEGERGAVLOGEYLG-QKAVAKNKR-CDTVAQAFDETAVMTKHOHENLYRLLG 293
Db 268 RLEVKGQGCGEWMGTYPSNVYAPSDSQAE-----EWFG 327
Qy 268 RLEVKGQGCGEWMGTYPSNVYAPSDSQAE-----EWFG 327
Db 294 VILHQGLYTMEHVKSGKLNVLFLTRGRALVNTAQOLQFLSHVAEGMELAESKKLVHDL 353
Qy 318 WVSERPIVYIEYMSKSLDPLKGMKYLRLPQVDMQAQIASGMAYVERMVYHDL 387
Db 354 AARNLIVSEDIVAKVSDFGIKA---ERKGLDSRSLPVKWTAPPALKHGKFTSKDWWS 409
Qy 388 RAANLIVGENLVEKQADFLGLARLIEDNEYTARQGAKFPKIKTAPEALYGRFTKSDWS 447
Qy 410 FGVLQMEYEVSGRAYQPKMSLKEVSEAVCGYRMMPEPGCPGPVHMLSSCWEAEPARRP 469
Db 448 FGILQLETLTGRGVYPMNREVIDQVERGYRMCCPPBCEPESLIDIMOCWRKQPEERP 507
Qy 470 PFRKLAELKARELRSAGAPASVGODAGSTSPPRSQ 505
Db 508 TFEVQLOAFL-----EDYFSTEPQXQ 528
Result 15
TVFVG0 1
Prtein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 22-May-1981 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
C;Accession: A38017; A00631; S02726; A38018
R;Czerniolsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Rischner, E.; Goodman, N.; Takeya, T.; Hanafusa, H.
A;Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
A;Reference number: A38017; MUID:83141780; PMID:6298633
A;Accession: A38017
A;Molecule type: DNA
A;Residues: 1-526 <CZE>

Tue Jul 29 11:52:07 2003

us-09-977-261-2.rpr

Page 10

QY 410 FGVLILWEVSYGRAYPKMSLKEYSEAVGYRMEPPPECOPGPVPHVLMSCWEAREPAPRP 469
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 448 FGILLETLTRKGRVYPGPGMNGEVLDYRGRMPCCPCPESLHDLMCQWRDPEERP 507

QY 470 PFRKLAEKL 478
| : |
Db 508 TFEYLOAQL 516

Search completed: July 29, 2003, 09:53:03
Job time : 25 secs

Page 1

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: July 29, 2003, 09:51:02 ; Search time 27 Seconds
Scoring table: (without alignments)
2230.045 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRSGLVSWRAFHGCDSE.....PASVSGQDADGSTSPRSQEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 11875970 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/podata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/podata/2/pubpaa/us06_NEW_PUB.pep:*

4: /cgn2_6/podata/2/pubpaa/us05_PUBCOMB.pep:*

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18: /cgn2_6/podata/2/pubpaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	2671	100.0	507	10 US-09-977-260-2
3	2671	100.0	507	11 US-09-977-261-2
4	1245.5	46.6	450	9 US-09-977-269-7
5	46.6	450	10	US-09-977-260-7
6	1245.5	46.6	450	11 US-09-977-261-7
7	1245.5	46.6	450	15 US-10-059-585-42
8	46.6	450	15	US-10-177-293-88
9	1245.5	46.6	450	16 US-10-298-377A-2
10	916	34.3	357	11 US-09-929-266-9
11	768	28.8	258	10 US-09-840-704-3
12	742.5	27.8	509	9 US-09-977-269-18
13	742.5	27.8	509	10 US-09-977-260-18
14	24.5	27.8	509	11 US-09-977-261-18
15	727	27.2	536	9 US-09-977-268-13

RESULT 1

US-09-977-269-2

Sequence 2, Application US-09977269

Patent No. US20020082037A1

GENERAL INFORMATION:

APPLICANT: ULMRICH, AXEL

APPLICANT: GISHIZKY, MTHAIL

APPLICANT: SURES, IRMINGARD

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

FILE REFERENCE: 038602/1260

CURRENT APPLICATION NUMBER: US-09-977, 269

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 08/232, 545

PRIOR FILING DATE: 1994-04-22

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 507

TYPE: PRT

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte

OTHER INFORMATION: Kinase 1

Query Match Best Local Similarity 100.0%; Score 2671; DB 9; Length 507; Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Best Local Similarity 100.0%; Score 2671; DB 9; Length 507; Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGRSGLVSWRAFHGCDSEELPLRVSPRLRWRWIPPSARMPTRWRPGTQCITKCEIT

Db 1 MAGRSGLVSWRAFHGCDSEELPLRVSPRLRWRWIPPSARMPTRWRPGTQCITKCEIT

QY 61 RPKGELAFRKGDWVILEACENKSWYRKHHSQEGLLAGALREREALSADPKLSM

Db 61 RPKGELAFRKGDWVILEACENKSWYRKHHSQEGLLAGALREREALSADPKLSM

QY 121 PWFGKISQEAQOLQPPEGGFLVRESARHPDYVLQVSFGRDVIVHVRVLHDGHLT

NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 7
 LENGTH: 450
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-977-261-7

Query Match 46.6%; Score 1245.5; DB 11; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTCITKCEHTRPKPGELAERKGDVYTLAREENSMWYRKHHTSQEGGLIAAGALR 105
 Db 8 WPMSGTECIAKYNFHGTABODLPCKGDYLTVTAVTKPDNWYKAKNV-GREGIIPANYVO 66

Qy 107 EREALSADPKLSLMPWFGKISQEAQVQLQPPEDGLFLVRESARHPGDYVLCVSFRDV 166
 Db 67 KREGVYKAGTKLSQLMPWFGKITEQAERLLYPPETGLELVRSESTNPGDYTLCSICDGKV 126

Qy 167 HYRVLHRDGHLTIDEAVFFCNLMDMVEHYSKDKGAICTKLYPRKRKGTKSAEELARA 226
 Db 127 EHRYIMYHASKLUSIDEEVYFENLMQLVHEHTSDADGLCITRLIKPKVMEGTVAODEYRS 186

Qy 227 GWLLNLQHLTGAQGEFGAVIQLQEGLGQKAWKNIKCDVTAQAFDETAWMKHO 286
 Db 187 GWALNMKEELKLQLQTICKGEFDVMLGDRYGRKVKCITKLYPRKRKGTKSAEELARA 226

Qy 287 NLVRLIGVILHQ - GLYIYMEHYSKKGNLYNLFRTGRALVNTAQOLQFSLHVADGEMYLE 344
 Db 247 NLVQLIGVIVEEKGYLYVTEYAKSGLVDYLASGRSLVGGDCLIKSFSLDVCAEMLYE 306

Qy 345 SKRLVHDLAARNILYSEDLVAKVSDFGLAKAERKGKLOSSRLPVWTPEALKHGKFTSK 404
 Db 307 GNMFVHRDLAARNVLVSNDNAVKVSDFGLKTEASSTDGTGKLPVWTPEALREKKSTK 366

Qy 405 SDWWSFGVLLWEEFSYGRAPYPKMSLKEVSEAVEKGYRMEEPGCCPGPHVLMSSCWEA 464
 Db 367 SDWWSFGVLLWEEFSYGRVYPYRPLKDVPVREKGYKMDADPGCPPAVYEVNKNCWHLD 426

Qy 465 PARRPFPKLAEL 478
 Db 427 AMMRSPFLQLRQL 440

RESULT 7
 US-10-059-585-42
 Sequence 42, Application US/10059585
 Publication No. US20030082776A1

GENERAL INFORMATION:
 APPLICANT: Ota, Toshio
 APPLICANT: Isogai, Takao
 APPLICANT: Nishikawa, Tetsuo
 APPLICANT: Hayashi, Koji
 APPLICANT: Otsuka, Kaoru
 APPLICANT: Yamamoto, Jun-ichi
 APPLICANT: Ishii, Shizuko
 APPLICANT: Sugiyama, Tomoyasu
 APPLICANT: Wakamatsu, Ai
 APPLICANT: Nagai, Keiichi
 APPLICANT: Otsuki, Tetsuji
 APPLICANT: Funahashi, Shin-ichi
 APPLICANT: Senoo, Chiaki
 APPLICANT: Nezu, Jun-ichi
 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 FILE REFERENCE: 06501-098001
 CURRENT FILING DATE: 2002-01-29
 PRIOR APPLICATION NUMBER: PCT/JP00/05060
 PRIORITY FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US 60/183, 322
 PRIORITY FILING DATE: 2000-02-17

Query Match 46.6%; Score 1245.5; DB 15; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTCITKCEHTRPKPGELAERKGDVYTLAREENSMWYRKHHTSQEGGLIAAGALR 105
 Db 8 WPMSGTECIAKYNFHGTABODLPCKGDYLTVTAVTKPDNWYKAKNV-GREGIIPANYVO 66

Qy 107 EREALSADPKLSLMPWFGKISQEAQVQLQPPEDGLFLVRESARHPGDYVLCVSFRDV 166
 Db 67 KREGVYKAGTKLSQLMPWFGKITEQAERLLYPPETGLELVRSESTNPGDYTLCSICDGKV 126

Qy 167 HYRVLHRDGHLTIDEAVFFCNLMDMVEHYSKDKGAICTKLYPRKRKGTKSAEELARA 226
 Db 127 EHRYIMYHASKLUSIDEEVYFENLMQLVHEHTSDADGLCITRLIKPKVMEGTVAODEYRS 186

Qy 227 GWLLNLQHLTGAQGEFGAVIQLQEGLGQKAWKNIKCDVTAQAFDETAWMKHO 286
 Db 187 GWALNMKEELKLQLQTICKGEFDVMLGDRYGRKVKCITKLYPRKRKGTKSAEELARA 226

Qy 287 NLVRLIGVILHQ - GLYIYMEHYSKKGNLYNLFRTGRALVNTAQOLQFSLHVADGEMYLE 344
 Db 247 NLVQLIGVIVEEKGYLYVTEYAKSGLVDYLASGRSLVGGDCLIKSFSLDVCAEMLYE 306

Qy 345 SKRLVHDLAARNILYSEDLVAKVSDFGLAKAERKGKLOSSRLPVWTPEALKHGKFTSK 404
 Db 307 GNMFVHRDLAARNVLVSNDNAVKVSDFGLKTEASSTDGTGKLPVWTPEALREKKSTK 366

Qy 405 SDWWSFGVLLWEEFSYGRAPYPKMSLKEVSEAVEKGYRMEEPGCCPGPHVLMSSCWEA 464
 Db 367 SDWWSFGVLLWEEFSYGRVYPYRPLKDVPVREKGYKMDADPGCPPAVYEVNKNCWHLD 426

Qy 465 PARRPFPKLAEL 478
 Db 427 AMMRSPFLQLRQL 440

RESULT 8
 US-10-177-293-88
 Sequence 88, Application US/10177-293
 Publication No. US20030124128A1

GENERAL INFORMATION:
 APPLICANT: Lillie, James
 APPLICANT: Glatt, Karen
 APPLICANT: Zhao, Xumei
 APPLICANT: Gannavarapu, Manjula
 APPLICANT: Kamatkar, Shubhangi
 APPLICANT: Mertens, Maureen
 APPLICANT: Myer, Vic
 APPLICANT: Wang, Youzhen
 APPLICANT: Xu, Yongyao
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Monahan, John
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Bast, Jr., Robert C.
 APPLICANT: Hortobagyi, Gabriel N.
 APPLICANT: Puszai, Lajos

```

APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE REFERENCE: MRT-038
CURRENT APPLICATION NUMBER: US10/177,293
CURRENT FILING DATE: 2005-06-21
; PRIORITY APPLICATION NUMBER: US 60/299,887
; PRIORITY FILING DATE: 2001-06-21
; PRIORITY APPLICATION NUMBER: US 60/301,572
; PRIORITY FILING DATE: 2001-06-27
; PRIORITY APPLICATION NUMBER: US 60/306,501
; PRIORITY FILING DATE: 2001-07-18
; PRIORITY APPLICATION NUMBER: US 60/325,002
; PRIORITY FILING DATE: 2001-09-25
; PRIORITY APPLICATION NUMBER: US 60/362,585
; PRIORITY FILING DATE: 2002-03-05
; PRIORITY APPLICATION NUMBER: US 60/305,511
; PRIORITY FILING DATE: 2002-05-14
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO: 88
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-177-293-88

Query Match          46.6%; Score 1245.5; DB 15; Length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
QY 47 WAPGTCITCKCEHTRPKPGELAFRKGDWVTLAECKNSWYRKHHTSGOEGLLAAGALR 106
Db 8 WPSGTCIACKYNFHGTAEDQDPLFCKGDKDVLTIVATKDPWNWAKNNV-GREGITPANYQ 66
QY 107 EREALSADPKSLMPWFHGKISGQBAVQQQLOPPEDGLFLYRESARHPGDYVLCVSFGRDV 166
Db 67 KREGVAGTKSLMPWFHGKTRTQAERLIPPETGFLFLVRESTNPYPGDYLTCVSCDGKV 126
QY 167 IHYRHHRDHGLTIDEAVFCNLMDMVEYSKDGAICTKLVRKRKHGTSAEELARA 226
Db 127 EHRYTMWHASKLISDEVYENLMLQLEVHTSDADGLCTRLIKPKVMEGTVAQDEFYRS 186
Db 127 EHRYTMWHASKLISDEVYENLMLQLEVHTSDADGLCTRLIKPKVMEGTVAQDEFYRS 186
QY 227 GWLNLIQHHTIGAQIGEGERGAVLQGEYLQOKVAKNIKDVTQAFDETAWMKMQHE 286
Db 187 GWALNKKELKLQLQTIGKGFERGDDVMDYQNGNKAVKCIKNDATAQFLAASVTOQLRHS 246
QY 287 NLVRLLGVILHQ- GLYIVMEHVSKGNLVFLTRGRALVNTAQQLQFSHLVAEGMEYLE 344
Db 247 NLVQLQGVIVEKGGLIVTEYMAKGSVLVDYLLRSRGRSVLGCDCLIKFSLDVCAMEYLE 306
QY 345 SKKLVRDLAARNLIVSEDIVAKVSDFGLKAERKGKLDSSRLPKWTAPEALKFKFTSK 404
Db 307 GNFEVFRDLAARNLVLEDNAVKVSDFGLKAESSTDQTSKLPWKWTAPEALKFKFTSK 366
QY 405 SDWWSFGVILWEVFSYGRAPYKMSKEVSEAVKGYRMEPPEGCPGPVHLMSSCWEAE 464
Db 367 SDWWSFGVILWEVFSYGRAPYKMSKEVSEAVKGYRMEPPEGCPGPVHLMSSCWEAE 426
QY 465 PARRPFKRKAEKL 478
Db 427 AAMRPSFLQREQL 440

RESULT 9
US-10-298-377A-2
; Sequence 2, Application US10/298377A
; Publication No. US20030130209A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Cheresh, David A.
; APPLICANT: Paul, Robert

RESULT 10
US-05-929-266-9
; Sequence 9, Application US/09929266
; Publication No. US20030045694A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matressich

```

APPLICANT: Kevin J. McConnel
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173.000302
CURRENT APPLICATION NUMBER: US/09/929 266
CURRENT FILING DATE: 2001-08-13
PRIORITY FILING DATE: 2000-08-11
PRIORITY APPLICATION NUMBER: 60/224, 939
PRIORITY FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 357
TYPE: PRP
ORGANISM: Homo sapiens
SEQ ID NO 9-929-266-9

Query Match 34.3% Score 916; DB 11; Len 357
Best Local Similarity 52.3%; Pred. No. 26-66; Mismatches 97; In
Matches 183; Conservative 62; MisMatches 97; In
Length 357

47 WAPGTCQCTTCEHTTRPKGEELAFRKGDWTILEACENNSWYRN
8 WPGTECIAKYNFHGTAEQDQLPCKGDVLTIAVTKDNEWYKA
107 EREALSAPKLSMPWFEGKISQEAVQLOQPPEDGLEFLYRSS
111 : | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
127 EHRYGVAKTKLSLMPWFHGKTRQAERLILYPETGLFLVREES
67 KRGVKGAKTKLSLMPWFHGKTRQAERLILYPETGLFLVREES
167 IYRVLHRDGHLTIDEAVFFCNLMDDMVEHYSKOGKATCTKLYF
111 : | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
227 GWLNLQHNLTLGAQIGECEFGAVLQGEFLQGKAVKNKCDYV
187 GWAJNMKERKLLOTIGKEGFDVMGLDGRGNKVKCIKNDAT
287 NLVRLLGYLTHO--GLYVMEHVSKGNVNFLETRGRALVNFT
111 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
247 NLVQLLGGVVIEEKGGLYLVTEXMAKGSLLVDYLSRGRSGVLLGG
345 SKKLYHROLAARNILVSDLDLVAKVSDGFLAK---RERKGIL
111 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
307 GNNFVRDLDAAVNVLSPDNVAKVSDGFLKTEASTPRRASCC
-S-09-840-004-3

Sequence 3, Application US/098440704
Patient No. US20020122801A1
GENERAL INFORMATION:
APPLICANT: Deehan, Shoukat
APPLICANT: Hannigan, Greg
TITLE OF INVENTION: Integrin-Linked Kinase and its Use
FILE REFERENCE: KN-2CON
CURRENT APPLICATION NUMBER: US/09/840, 704
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/556, 906
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US08/752, 345.
PRIOR FILING DATE: 1996-11-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 258
TYPE: PRP
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: Other
LOCATION: (1)...(258)
-09-840-004-3

Best Local Similarity 58.8%; Pred. No. 1.4e-54; Matches 147; Conservative 45; Mismatches 56; Indels 2; Gaps 1;

QY 231 NLQHHTLGAQIGEGEFGAVLQGEGVYKAVAKIKCDVTAQFDETAVMTKHOHENIYR 290
Db 1 NKKELKLQIOTICKGERGDVMLGDYRGKVKACIKNDATAQAFLEASVNTOLRHSNLVO 60

QY 291 LLGVHQ -GLIVVMWVKSGNVLNLTGRGLVNLNTAQLQFSHLHAEGMFLLESKL 348
Db 61 LLGVVTEEEKGYLVTHYMAKSLSVDLRSRGRSVLGDCLLRSRSLDVECEAMELEGNNF 120

QY 349 VHRDLAARNLTVSEEDLAVKVSDFGLAKAERKGKGDLSRLPVKWAPEALKHGKFPSKSDW 408
Db 121 VRDLAARNLTVSEEDLAVKVSDFGLAKAERKGKGDLSRLPVKWAPEALKHGKFPSKSDW 180

QY 409 SFGVLIVMEVFSGRAPPKMSLUKEVSEANVEGYMRPEPGCOPPHVUMSSCRAEPAAR 468
Db 181 SFGVLIVMEVFSGRAPPKMSLUKEVSEANVEGYMRPEPGCOPPHVUMSSCRAEPAAR 240

QY 469 PPFKLAEKL 478

Db 241 PSFLQREQL 250

RESULT 12
US-03-977-269-18

; Sequence 18, Application US/09977269
; Patent No. US20020082037A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISIHKY, MIKHAIL
; APPLICANT: SURES, TRINAGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977, 269
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232, 545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-977-269-18

Query Match 27.8%; Score 742.5; DB 9; Length 509;
Best Local Similarity 37.6%; Pred. No. 4e-52; Mismatches 155; Indels 25; Gaps 9; Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;

QY 65 GELAFRKGDVVVTLAECKENSKWYRKHHTSGOEGGLANGALRERFEALSADPKLSSLMPWFH 124
Db 78 GDLGFEKGEQLRILE--QSGEWKAQASLTGQEGFIPENFVAKNSLEP-----PNF 129

QY 125 GKISQEAQVQQLQPED--GLFLVRESARHPGDYLVCV----SFGRDVIVHYRLHD-G 176
Db 130 KNLSRKDAERQQLAPGWTGHSELRESESTAGSLSLSDRFEDONQEVWVKHYRLNG 189

QY 177 HLTIDEAVFFCNMUDWHEYSKDQGATCKLVRPKRKHGKTSAAEELARAGWLNLQHLT 236
Db 190 GFYISRTRTPGQLHLMVRHYTNAASDGCLTRSPCQ--TORKQPKWNEDEWEVPRELIK 246

QY 237 LGAQIGEGEFGAVLQGEGVYKAVAKIKCDVTAQFDETAVMTKHOHENIYR 294
Db 247 LVERLGAGQFGEWWMGYGTYNGHTRKVAVKSKLQGSMSPDAFLAKNLKQLOHORVRLVAY 306

QY 295 ILHQGIXYVMEHVSKGMVNLFRLTRGRALVNTAQQLQFSLHVAGMEYLESKKLVHDLA 354
Db 307 VTQEPYIYIETYMEGNSLVDLKTPSGIKLTINKLDMQAQJAEGMFIEERVYIHRDL 365

QY 355 ARNIIVSLEDIVAKVSPFLAKA---BRKGLOSSRLPVKWTAAPEALKKGFKTSKSDW 410
Db 367 AANTLIVSDTLACKSKIDAEGLARLIEDDNYTYRSGAKFPKWTAEAINGTFTKSDW 426

TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-977-269-13

Query Match Similarity Score 27.2%; Best Local Similarity 35.2%; Score 727; Length 536;
 保守性 83; Predicted No. 7.8e-51; Mismatches 178; Indels 74; Gaps 14;
 Matches 182;

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Qy 37 PVSA---RMPTRRWAP-----GROCITKCEHTRPKPG----- 65
Db 41 PASADCHRGPSAAFAAEPKLFFGGFNSSDPTVSPORAGPLAGGVTTVALDYERSRTE 100
Qy 66 -ELAFRKGDYVTILEACENKSWYRKKHHSQEGIAGALRERALSADPKLUSMPWPH 124
Db 101 TDLSFRKKGERLQIVNTEG-DWWLAHSLSTGOTGYIPSNVAPSNSIQAE-----EWTF 153
Qy 125 GKIQSQEAVQOLQPED-GFLFVRESARAHGDYVLCVS---FGRDVHYRLHRD-G 176
Db 154 GKTRRESERULLNAENPRGTFLYRESEETKGAVCLSVDFDNAGLNKHYKRKLDG 213
Qy 177 HLTIDBAVFTCNLMQDVHEYSKDKGAICTKL-VRPKRKGTKSAAEEELARAGWLNLOH 234
Db 214 GFYITSRTQFNSLQOLVAVYKSHADGLCHRLLTVOPTSKPQTG---LAKDANEIPRES 269
Qy 235 LTIGAQIGEBCERFGAVLOGEGLG-DRVAVNIK-CDVTAQFLDEPAWMKMOHENLVRL 292
Db 270 LRLEVLRKGQCGFGEVWWMGTWNGTRVAIKTLKPGTMSPEAFLOEQNMKRLRERKVLY 329
Qy 293 GVILHQGLYIYMERHKSGNLYNLFTRGRALVNRAQLOFSLHVREGMYESKLVHBD 352
Db 330 AVVSEBPIYTVEYMSKGSLIDFLKGETGKYLRPLQVLMQAQIASGMAYVERMYVHD 389
Qy 353 LAARNILVSELDLVAKVSDSGLAKA---PERKGLDSSRLPKWTAAPEALTHKGKFTSKDW 408
Db 390 LRAANILVGENLNUCKVADQGLARLIEDNEYTARQGAKFPKWTAAPEALHYGRFTIKSDW 449
Qy 409 SFGVILWEVESYGRAPYKHSILKEYSEAVERGYRNEPPGCPGPVPHVLLSSCWAEPAR 468
Db 450 SFGILLTLELTGKRYVYPGAVNRLEVDQVERGYRNPCCPPECPESELHDMQCWRKEPEER 509
Qy 469 PPFRLKLAEKARELJSAGIAPASVSCQDAGSTSRQ 505
Db 510 PTFEYLQAFL-----EDYFTSTEPOYQ 531

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Search completed: July 29, 2003, 09:53:36
 Job time : 29 secs

GenScore Version 5.1.6
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DM protein - protein search, using sw model

Run on: July 29, 2003, 09:49:12 ; Search time 20 Seconds

Sequence: (without alignments) 1 MAGRGLSVWRAFHGCD\$AB....., PAVSQGQDAGGSTSPRSQEP 507

Database: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42210858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCGTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2671	100.0	507 4 US-08-426-509A-2	Sequence 2, Appli
2	2671	100.0	507 4 US-08-426-509A-2	Sequence 2, Appli
3	2671	100.0	507 5 PCT-US95-05008-2	Sequence 2, Appli
4	2664	99.7	507 2 US-08-604-989A-5	Sequence 5, Appli
5	2445	91.5	527 4 US-09-315-928-2	Sequence 2, Appli
6	2444	91.5	466 2 US-08-604-989A-4	Sequence 2, Appli
7	2434.5	91.1	528 2 US-08-870-8882-2	Sequence 2, Appli
8	2012	75.3	386 4 US-09-741-154-2	Sequence 4, Appli
9	2012	75.3	415 4 US-09-741-154-2	Sequence 4, Appli
10	1269	47.5	246 2 US-08-604-989A-3	Sequence 3, Appli
11	1245.5	46.6	450 4 US-08-426-509A-4	Sequence 7, Appli
12	1245.5	46.6	450 5 PCT-US95-05008-7	Sequence 7, Appli
13	1245.5	46.6	450 5 US-09-039-555B-17	Sequence 7, Appli
14	797	29.8	269 3 US-08-701-191A-35	Sequence 35, Appli
15	768	28.8	258 3 US-09-035-706-3	Sequence 2, Appli
16	768	28.8	258 3 US-08-95-841-3	Sequence 3, Appli
17	768	28.8	258 4 US-09-310-425-3	Sequence 7, Appli
18	768	28.8	258 4 US-09-566-906-3	Sequence 7, Appli
19	742.5	27.8	509 3 US-09-039-555B-17	Sequence 7, Appli
20	742.5	27.8	509 4 US-08-426-509A-18	Sequence 18, Appli
21	742.5	27.8	509 4 US-09-457-040B-8	Sequence 3, Appli
22	742.5	27.8	509 4 US-08-232-545-18	Sequence 3, Appli
23	742.5	27.8	509 5 PCT-US95-05008-18	Sequence 18, Appli
24	732	27.4	533 1 US-07-820-011A-2	Sequence 2, Appli
25	732	27.4	533 5 PCT-US93-00445-2	Sequence 2, Appli
26	27.2	536 1 US-07-820-011A-2	Sequence 4, Appli	
27	27.2	536 4 US-08-426-509A-13	Sequence 13, Appli	

ALIGNMENTS

RESULT 1	US-08-426-509A-2
SEQUENCE 2, Application	US/08426509A
Patent No.	6326469
GENERAL INFORMATION:	
APPLICANT:	Ulrich, Axel
APPLICANT:	Gishizky, Mihail
APPLICANT:	Sures, Iman G.
TITLE OF INVENTION:	NOVEL MEGAKARYOCYTIC PROTEIN
NUMBER OF SEQUENCES:	21
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Pennie & Edmonds
STREET:	1155 Avenue of the Americas
CITY:	New York,
STATE:	NY
COUNTRY:	USA
ZIP:	10036-2711
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Diskette
COMPUTER:	IBM Compatible
OPERATING SYSTEM:	DOS
SOFTWARE:	FASSEQ Version 2.0
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/426,509A
FILING DATE:	21-APR-1995
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/232,545
FILING DATE:	
ATTORNEY/AGENT INFORMATION:	
NAME:	Coruzzi, Laura A
REGISTRATION NUMBER:	30,742
REFERENCE DOCKET NUMBER:	7683-0074-999
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	212-790-9090
TELEFAX:	212-869-9741
TELEX:	66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:	
SEQUENCE CHARACTERISTICS:	
LENGTH:	507 amino acids
TYPE:	amino acid
STRANDEDNESS:	unknown
TOPOLOGY:	unknown
MOLECULE TYPE:	No. 6326469
US-08-426-509A-2	
Query Match	100.0%
Best Local Similarity	100.0%
Matches	0;
Indels	0;
Gaps	0;

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 24-APR-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: US 08/232,545
 FILING DATE: 22-APR-1994
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 507 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US95-05008-2

Query Match 100.0% Score 2671; DB 5; Length 507;
 Best Local Similarity 100.0%; Pred. No. 2,7e-219;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGRSLSVSWRAFGCDSAEELPRVSPrLRAWHPVSPRMPrRWAQTCITKCEHT 60
 Db 1 MAGRSLSVSWRAFGCDSAEELPRVSPrLRAWHPVSPRMPrRWAQTCITKCEHT 60

Qy 61 RPKGELAFRKGDVVTILEACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120
 Db 61 RPKGELAFRKGDVVTILEACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120

Qy 121 PWFHGKISQEAQVQOLQPPEPDGLTVRESARHPGDYVLCVSGFDVYIHRVLRHDGHLT 180
 Db 121 PWFHGKISQEAQVQOLQPPEPDGLTVRESARHPGDYVLCVSGFDVYIHRVLRHDGHLT 180

Qy 181 DEAVFFCNLMDFVEHYSKKGAICTKLVRPKRKHGTSKEELARAGWLNLQHLTGAQ 240
 Db 181 DEAVFFCNLMDFVEHYSKKGAICTKLVRPKRKHGTSKEELARAGWLNLQHLTGAQ 240

Qy 241 IGEGERGAVLQGEYQKVAKNPKCDVTAQAFQLEDETAWTMKMOHENLYRLGVLTHQGL 300
 Db 241 IGEGERGAVLQGEYQKVAKNPKCDVTAQAFQLEDETAWTMKMOHENLYRLGVLTHQGL 300

Qy 301 YIVMEHVKSGNLVNLRTRGALVNTAQQLQFSLHVAGEMEYLESKKLVHDLARNILV 360
 Db 301 YIVMEHVKSGNLVNLRTRGALVNTAQQLQFSLHVAGEMEYLESKKLVHDLARNILV 360

Qy 361 SEDLVAKVSDPGLAKAERKGDSLSPRVSPrLPAEALKHGFTSKSDWVSPGVHLWEVFSY 420
 Db 361 SEDLVAKVSDPGLAKAERKGDSLSPRVSPrLPAEALKHGFTSKSDWVSPGVHLWEVFSY 420

Qy 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKLR 480
 Db 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKLR 480

Qy 481 ELRSAGAPASVSGDADGTSPrSOEP 507
 Db 481 ELRSAGAPASVSGDADGTSPrSOEP 507

Query Match 99.8% Score 2664; DB 2; Length 507;
 Best Local Similarity 99.8%; Pred. No. 1e-218; 1; Mismatches 0; Indels 0; Gaps 0;

Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGRSLSVSWRAFGCDSAEELPRVSPrLRAWHPVSPRMPrRWAQTCITKCEHT 60
 Db 1 MAGRSLSVSWRAFGCDSAEELPRVSPrLRAWHPVSPRMPrRWAQTCITKCEHT 60

Qy 61 RPKGELAFRKGDVVTILEACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120
 Db 61 RPKGELAFRKGDVVTILEACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120

Qy 121 PWFHGKISQEAQVQOLQPPEPDGLTVRESARHPGDYVLCVSGFDVYIHRVLRHDGHLT 180
 Db 121 PWFHGKISQEAQVQOLQPPEPDGLTVRESARHPGDYVLCVSGFDVYIHRVLRHDGHLT 180

Qy 181 DEAVFFCNLMDFVEHYSKKGAICTKLVRPKRKHGTSKEELARAGWLNLQHLTGAQ 240

Qy 241 IGEGERGAVLQGEYQKVAKNPKCDVTAQAFQLEDETAWTMKMOHENLYRLGVLTHQGL 300

Qy 301 YIVMEHVKSGNLVNLRTRGALVNTAQQLQFSLHVAGEMEYLESKKLVHDLARNILV 360

Qy 361 SEDLVAKVSDPGLAKAERKGDSLSPRVSPrLPAEALKHGFTSKSDWVSPGVHLWEVFSY 420

Qy 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKLR 480

Qy 481 ELRSAGAPASVSGDADGTSPrSOEP 507

Query Match 99.8% Score 2664; DB 2; Length 507;
 Best Local Similarity 99.8%; Pred. No. 1e-218; 1; Mismatches 0; Indels 0; Gaps 0;

Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGRSLSVSWRAFGCDSAEELPRVSPrLRAWHPVSPRMPrRWAQTCITKCEHT 60
 Db 1 MAGRSLSVSWRAFGCDSAEELPRVSPrLRAWHPVSPRMPrRWAQTCITKCEHT 60

Qy 61 RPKGELAFRKGDVVTILEACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120
 Db 61 RPKGELAFRKGDVVTILEACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120

Qy 121 PWFHGKISQEAQVQOLQPPEPDGLTVRESARHPGDYVLCVSGFDVYIHRVLRHDGHLT 180
 Db 121 PWFHGKISQEAQVQOLQPPEPDGLTVRESARHPGDYVLCVSGFDVYIHRVLRHDGHLT 180

Qy 181 DEAVFFCNLMDFVEHYSKKGAICTKLVRPKRKHGTSKEELARAGWLNLQHLTGAQ 240

Qy 241 IGEGERGAVLQGEYQKVAKNPKCDVTAQAFQLEDETAWTMKMOHENLYRLGVLTHQGL 300

Qy 301 YIVMEHVKSGNLVNLRTRGALVNTAQQLQFSLHVAGEMEYLESKKLVHDLARNILV 360

Qy 361 SEDLVAKVSDPGLAKAERKGDSLSPRVSPrLPAEALKHGFTSKSDWVSPGVHLWEVFSY 420

Qy 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKLR 480

Qy 481 ELRSAGAPASVSGDADGTSPrSOEP 507

RESULT 4
 US-08-604-989A-5
 ; Sequence 5, Application US/08604989A

RESULT 5
US-09-315-928-2

; Sequence 2, Application US/09315928
; Patent No. 6368796

; GENERAL INFORMATION:
; APPLICANT: Avraham, Hava
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: BREAST CANCER
; FILE REFERENCE: NED97-01PAZ
; CURRENT APPLICATION NUMBER: US/09/315, 928
; CURRENT FILING DATE: 1999-05-20
; PRIORITY NUMBER: US 08/876, 882
; PRIORITY NUMBER: US 60/035, 228
; PRIORITY FILING DATE: 1997-01-08
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-315-928-2

Query Match 91.5%; Score 2445; DB 4; Length 527;
Best Local Similarity 93.5%; Pred. No. 4.9e-200; Matches 472; Conservative 1; Mismatches 18; Indels 14; Gaps 2;

QY 1 MAGRGSLSWRAFGCDSSKEELPVRSPRLTRWPPVARMPPRWRAGTCTKCEIT 60
1 MAGRGSLSWRAFGCDSSKEELPVRSPRLTRWPPVARMPPRWRAGTCTKCEIT 60

QY 61 RPKPGELAPRKGDVVTILEACENSKWYRKHTSGQEGLLAAGALRDGEALSADPKLSM 120
61 RPKPGELAPRKGDVVTILEACENSKWYRKHTSGQEGLLAAGALRDGEALSADPKLSM 120

QY 121 PWHGKISQEAQVQLQPEDFGLYFLVRESARHPHGDVYLCSFGDHWYVRLVLRDGHLT 180
121 PWHGKISQEAQVQLQPEDFGLYFLVRESARHPHGDVYLCSFGDHWYVRLVLRDGHLT 180

QY 121 DEAVFCNLMDMVHYSKDKGAICTKLVRPKRGTKSAEEELARAGWLNLQHILGQ 240
121 DEAVFCNLMDMVHYSKDKGAICTKLVRPKRGTKSAEEELARAGWLNLQHILGQ 240

QY 241 TGRSEFGAVLQGETLGQKVAKNPKCDVTAQAFQDLETAVMTKMOHENLVRLLSYTLHGL 300
241 TGRSEFGAVLQGETLGQKVAKNPKCDVTAQAFQDLETAVMTKMOHENLVRLLSYTLHGL 300

QY 241 IGGEGFAGVLQGETLGQKVAKNPKCDVTAQAFQDLETAVMTKMOHENLVRLLSYTLHGL 300
241 IGGEGFAGVLQGETLGQKVAKNPKCDVTAQAFQDLETAVMTKMOHENLVRLLSYTLHGL 300

QY 301 YTMHEVHSQGNLNFLRTRGRALVNTAQQLQFSHLVAEGMEYLESKLVLHDLAARNLIV 360
301 YTMHEVHSQGNLNFLRTRGRALVNTAQQLQFSHLVAEGMEYLESKLVLHDLAARNLIV 360

QY 361 SEDLWAKSDFGLAKAERKGKDLSRSLPKWTAEALKHQKFTSKDSVNSFGVLLWEVFSY 420
361 SEDLWAKSDFGLAKAERKGKDLSRSLPKWTAEALKHQKFTSKDSVNSFGVLLWEVFSY 420

QY 420 GRAPYPKMSIKEVEAVERGVYRMPPECGCPGPVHLMSSCWEAPPAGHP----- 469
420 GRAPYPKMSIKEVEAVERGVYRMPPECGCPGPVHLMSSCWEAPPAGHP----- 469

QY 481 ELSAGAPASVSGODAGSTSPSQ 505
481 ELSAGAPASVSGODAGSTSPSQ 505

QY 470 --SANWPRSWPGSYAVVOPPSQ 491
470 --SANWPRSWPGSYAVVOPPSQ 491

RESULT 5
US-06-604-9894-4

; Sequence 4, Application US/08604989A
; Patent No. 5834208

; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: NO. 5834208e1 Tyrosine Kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604 989A
; FILING DATE: February 23, 1996
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Charles E. Miller
; REGISTRATION NUMBER: 24, 576

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 6611 PENNIE

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:
; ORGANISM: human

; STRAIN: UT-7

US-06-604-9894-4

Query Match 91.5%; Score 2444; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 5e-200; Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MPTRWAWPGTCITKCEHTRPKGELAPRKGDVVTILEACENSKWYRKHTSGQEGLLA 101
1 MPTRWAWPGTCITKCEHTRPKGELAPRKGDVVTILEACENSKWYRKHTSGQEGLLA 60

QY 102 AGALREREALSDAPKLSLMPWFHGKTSQEARVQQLQPEDGFLYFLVRESARHPGDVYLCS 161
61 AGALREREALSDAPKLSLMPWFHGKTSQEARVQQLQPEDGFLYFLVRESARHPGDVYLCS 120

QY 162 FGDRDVYHVRDGHLTIDEAVFCNLMDMVHYSKDKGAICTKLVRPKRGTKSAEE 221
121 FGDRDVYHVRDGHLTIDEAVFCNLMDMVHYSKDKGAICTKLVRPKRGTKSAEE 180

QY 222 BLARAGWLNLQHILGQAZQEGEGEGAVLQGYLGQKVAKNIKCDVTAQAFQDLETAVMT 281

QY 342 YLESKKVLVRDGLAARNLIVSLEDLWAKSDFGLAKAERKGKDLSRSLPKWTAEALKHQKFTSKDSVNSFGVLLWEVFSY 401
342 YLESKKVLVRDGLAARNLIVSLEDLWAKSDFGLAKAERKGKDLSRSLPKWTAEALKHQKFTSKDSVNSFGVLLWEVFSY 401

QY 301 YLESKKVLVRDGLAARNLIVSLEDLWAKSDFGLAKAERKGKDLSRSLPKWTAEALKHQKFTSKDSVNSFGVLLWEVFSY 360
301 YLESKKVLVRDGLAARNLIVSLEDLWAKSDFGLAKAERKGKDLSRSLPKWTAEALKHQKFTSKDSVNSFGVLLWEVFSY 360

QY 402 TSKDWWSFGVLLWEVFSYGRAPYPKMSIKEVEAVERGVYRMPPECGCPGPVHLMSSCWEAPPAGHP----- 461
402 TSKDWWSFGVLLWEVFSYGRAPYPKMSIKEVEAVERGVYRMPPECGCPGPVHLMSSCWEAPPAGHP----- 461

RESULT 7
 US-08-876-882-2
 ; Sequence 2, Application US/08876882
 ; Patent No. 5981201
 ; GENERAL INFORMATION:
 ; APPLICANT: Avraham, Hava
 ; APPLICANT: Groopman, Jerome E.
 ; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
 ; TITLE OF INVENTION: OF BREAST CANCER
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173-4799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/876, 882
 FILING DATE: 16-JUN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/035, 228
 FILING DATE: 08-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Doreen, Rogie M
 REFERENCE/DOCKET NUMBER: 36-361
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 528 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 ; US-08-876-882-2

Query Match Best Local Similarity 93.3%; Score 2434.5; DB 2; Length 528; Matches 472; Conservative 1; Mismatches 18; Indels 15; Gaps 3;

QY 1 MAGRGLSVSRRAFGCDSAAELPRLPRSPRFRAWHPPVPSARMPPRWRWAGPTQCTIKCET 60
 QY 1 MAGRGLSVSRRAFGCDSAAELPRLPRSPRFRAWHPPVPSARMPPRWRWAGPTQCTIKCET 60 .
 Db 1 MAGRGLSVSRRAFGCDSAAELPRLPRSPRFRAWHPPVPSARMPPRWRWAGPTQCTIKCET 60 .

QY 61 RPKPGELAFRKGDVVTIELAECAENKSWYRKHHTSGQEGILAAAGLREREALSDAPKSL 119
 QY 61 RPKPGELAFRKGDVVTIELAECAENKSWYRKHHTSGQEGILAAAGLREREALSDAPKSL 120

QY 120 MPWFHGKMSQEAVQLQPPEDGFLVREZARHPDGYVLCVSGFGRDVTHYVLRHDGHLT 179
 Db 120 MPWFHGKMSQEAVQLQPPEDGFLVREZARHPDGYVLCVSGFGRDVTHYVLRHDGHLT 179

QY 121 IDEAVFFCNLMDMVBHYSKQGAICTKLVPKRKIGTKSAEELARAGWLNLQHITGA 180
 Db 121 IDEAVFFCNLMDMVBHYSKQGAICTKLVPKRKIGTKSAEELARAGWLNLQHITGA 180

QY 180 IDEAVFFCNLMDMVBHYSKQGAICTKLVPKRKIGTKSAEELARAGWLNLQHITGA 239
 Db 181 IDEAVFFCNLMDMVBHYSKQGAICTKLVPKRKIGTKSAEELARAGWLNLQHITGA 240

RESULT 8
 US-09-741-154-4
 ; Sequence 4, Application US/09741154
 ; Patent No. 6437110
 ; GENERAL INFORMATION:
 ; APPLICANT: BEASLEY, Ellen M et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES OF THESE
 ; FILE REFERENCE: CL001061
 ; CURRENT APPLICATION NUMBER: US/09/741,154
 ; CURRENT FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 386
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-741-154-4

Query Match Best Local Similarity 100.0%; Pred. No. 2.4e-163; Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Length 386:

QY 122 WPHGKTSQEAQVQLQPPEDGFLVREZARHPDGYVLCVSGFGRDVTHYVLRHDGHLT 181
 QY 122 WPHGKTSQEAQVQLQPPEDGFLVREZARHPDGYVLCVSGFGRDVTHYVLRHDGHLT 181 .
 Db 1 WPHGKTSQEAQVQLQPPEDGFLVREZARHPDGYVLCVSGFGRDVTHYVLRHDGHLT 60
 Db 61 EAVFCLNMDVNEHTSKDGACIICKVVRKRHKTSAAEELARAGWLNLQHITGAQI 60

QY 182 EAFFFCNLMDVNEHTSKDGACIICKVVRKRHKTSAAEELARAGWLNLQHITGAQI 241
 Db 61 EAVFCLNMDVNEHTSKDGACIICKVVRKRHKTSAAEELARAGWLNLQHITGAQI 241

QY 242 GEGERGAVLQGCVYLLGOKAVANIKCDVTAQAFDLDETAVMTHOHENLVLRLGVLHQLY 301
 QY 242 GEGERGAVLQGCVYLLGOKAVANIKCDVTAQAFDLDETAVMTHOHENLVLRLGVLHQLY 301 .
 Db 121 GEGERGAVLQGCVYLLGOKAVANIKCDVTAQAFDLDETAVMTHOHENLVLRLGVLHQLY 180

QY 302 IVMEVHSKGKGNVNELETRGRALVNTAQQLQFSLYAEGMEYLESKLVHRLAANILVS 361
 Db 181 IVMEVHSKGKGNVNELETRGRALVNTAQQLQFSLYAEGMEYLESKLVHRLAANILVS 240

QY 362 EDLVAKVSDFGLAKAERKGKDSSRLPVKWTPEALKHGKFTSKDSWWSFGULLWENFSYG 421
 Db 241 EDLVAKVSDFGLAKAERKGKDSSRLPVKWTPEALKHGKFTSKDSWWSFGULLWENFSYG 300

QY 422 RAPYKMSLKEVSEAVEKGYRMEPEPGCPGPVHJMSSCWEAEPARRPFRKLAKLARE 481
 Db 301 RAPYKMSLKEVSEAVEKGYRMEPEPGCPGPVHJMSSCWEAEPARRPFRKLAKLARE 360

QY 482 LRSAPASVSGODADGSTSPRSQP 507
 Db 361 LRSAPASVSGODADGSTSPRSQP 386

RESULT 9

US-09-741-154-2

Sequence 2, Application US/09741154

Patient No. 6437110

GENERAL INFORMATION:

APPLICANT: BEASLEY, Ellen M. et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: C1001061

CURRENT APPLICATION NUMBER: US/09/741-154

CURRENT FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 415

TYPE: PRT

ORGANISM: Human

US-09-741-154-2

Query Match 75.3%; Score 2012; DB 4; Length 415;
 Best Local Similarity 100.0%; Pred. No. 2.6e-163; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 WFGKISSEAOVQLQPDPGLEVLRESKRPDGYVLCVSGRDIYHVRVLHRDGLHTD 181

Db 30 WFHKISSEAOVQLQPDPGLEVLRESKRPDGYVLCVSGRDIYHVRVLHRDGLHTD 89

Qy 182 EAVFFCNLMDWENYISKDKGAIKCKLVLRERKRGTKSSEELARAGWLNQHILTGAQI 241

Db 90 EAEVFCNLMDWENYISKDKGAIKCKLVLRERKRGTKSSEELARAGWLNQHILTGAQI 149

Qy 242 GEGFRGAVI-QGEY-GQKVAVKNIKCDVTAQAFDETAVTMKMOHENLYRLGVLTQHGY 301

Db 150 GEGFRGAVI-QGEY-GQKVAVKNIKCDVTAQAFDETAVTMKMOHENLYRLGVLTQHGY 209

Qy 302 IVMERVKSKNLVNFLTRGRALVNTAQLQFSHLVAEGMEYLESKKLVHRD 361

Db 210 IVMERVKSKNLVNFLTRGRALVNTAQLQFSHLVAEGMEYLESKKLVHRD 269

Qy 362 EDLVAKVSIFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSNSDWSFGLVMEVSYG 421

Db 270 EDLVAKVSIFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSNSDWSFGLVMEVSYG 329

Qy 422 RAPPKMSKEVSEAVEKGYMRMEPEGCGPVLMLSSCWEAEPARRPPFKLAEKLAKE 481

Db 330 RAPPKMSKEVSEAVEKGYMRMEPEGCGPVLMLSSCWEAEPARRPPFKLAEKLAKE 389

Qy 482 LRSAGAPASVSGQDADGSTSPRSOEP 507

Db 390 LRSAGAPASVSGQDADGSTSPRSOEP 415

RESULT 10

US-08-604-989A-3

Sequence 3, Application US/08604989A

Patient No. 5834208

GENERAL INFORMATION:

APPLICANT: Sakanou, S.

TITLE OF INVENTION: NO. 58342081 Tyrosine Kinase

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604-989A

FILING DATE: February 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Charles E. Miller

REGISTRATION NUMBER: 24,576

REFERENCE/DOCKET NUMBER: 1920-026

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 6641 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: human

STRAIN: un-7

US-08-604-989A-3

Query Match 47.5%; Score 1269; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2.4e-100; Indels 0; Gaps 0;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 233 QHLLTGAQIGEGERGAVILOGEYLGQKVAVKNIKCDVTAQAFDETAVTMKMOHENLYRL 292

Db 1 QHLLTGAQIGEGERGAVILOGEYLGQKVAVKNIKCDVTAQAFDETAVTMKMOHENLYRL 60

Qy 293 GVILHQGLYIUMERVKSKNLVNFLTRGRALVNTAQLQFSHLVAEGMEYLESKKLVHRD 352

Db 61 GVILHQGLYIUMERVKSKNLVNFLTRGRALVNTAQLQFSHLVAEGMEYLESKKLVHRD 120

Qy 353 LAARNILVSEDLVAKVSDFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSNSDWSFGLVMEVSYG 412

Db 121 LAARNILVSEDLVAKVSDFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSNSDWSFGLV 180

Qy 413 LLMEVFSGRAPPKMSKEVSEAVEKGYMRMEPEGCGPVLMLSSCWEAEPARRPPFR 472

Db 181 LLMEVFSGRAPPKMSKEVSEAVEKGYMRMEPEGCGPVLMLSSCWEAEPARRPPFR 240

Qy 473 KLAEKL 478

Db 241 KLAEKL 246

RESULT 11

US-08-4-26-509A-7

Sequence 7, Application US/08426509A

Patent No. 6320449

GENERAL INFORMATION:

APPLICANT: Ulrich, Axel

APPLICANT: Gishizky, Mikhail

APPLICANT: Sures, Iman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

TITLE OF INVENTION: TYROSINE KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-869-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 450 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: NO. 6326469e

US-08-426-509A-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/732,545

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-050

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212)869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 7:

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;

Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2;

Matches 235; Conservative 81; STRANDEDNESS:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-232-545-7

RESULT 12

US-08-232-545-7

Sequence 7, Application US/08232545

; General Information:

; Applicant:

Applicant: Ulrich, Axel

; Applicant:

Applicant: Gishizky, Mikhail

; Applicant: Sures, Iman G.

Title of Invention: Megakaryocytic Protein Tyrosine

Number of Sequences: 21

Correspondence Address:

Pennie & Edmonds

RESULT 13

US-08-232-545-7

PCT-US95-05008-7

Sequence 7, Application PC/TUS9505008

; General Information:

Applicant: Sugen, Inc.

APPLICANT: 515 Galveston Drive
 APPLICANT: Redwood City, California 94063-4720
 APPLICANT: United States of America
 APPLICANT: Wissenschaften E.V.
 APPLICANT: Hoffgarten Str., 2
 Munchen 80539

APPLICANT: Germany
 TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine Kinases
 TITLE OF INVENTION: Kinases
 NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penne & Edmonds
 STREET: 1155 Avenue of the Americas
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 STATE: New York
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 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05008
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-074

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)790-9090
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 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US95-05008-7

Query Match 46 6%; Score 1245.5; DB 5; Length 450;
 Best Local Similarity 54.1%; Pred. No. 5.3e-98; Indels 3; Gaps 2;
 Matches 235; Conservative 81; Mismatches 115; Delins 3; Gaps 2;

QY 47 WAPGTCITKCEHTRPKPGEALFRKGDVVILEAGENKSYWRVKHTSQEGLLAAGAR 106
 Db ||:|| | ||| :| ||| ||| :||| :| ||| ||| :||| ||| :||| ||| :||| |||
 8 WPSGCFCLAKYNFHCTAEDLPCKGDKVLTIVAVYKDPWVYKAKNVY-SREGIPANVQ 66

QY 107 EREALSADPKLISLMPWFHKISGQARAVQDQLQPPEDGLELYRESARHPGQYVLCVSFGRDV 166
 Db ||:|| :| ||| ||| ||| :||| :| ||| ||| ||| :||| ||| :||| ||| :||| |||
 67 KREGVKAGIKLSLMPWFHKITREORERULIPPERGLFLVRESTNPQDYLCSDCGRV 126

QY 167 IHYRLHRCHLTLDEAVFCNLMDVHEVSKDKGAICTKLVRKRKHQSJKSAEELARA 225
 Db ||:|| :| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 127 EHRYMYHASKLSTIDEEVYFNPMOLVEHVTSDADGCLTKPRVMEGVVAODEFYRS 186

QY 227 GWLNLNQHLTIGAQIGEGERGAQVLOGEYQGQKAVKNKICDVQAQAFDETAVMKHQIE 286
 Db ||:|| :| ||| ||| :||| :||| ||| :||| :||| ||| :||| :||| :||| :|||
 187 GWALMKELKLQQTGKGERGQDMVGDYQNGKNAVKCINKDQAFQAEASVYMLRIS 245

QY 287 NLVRLLGVLVHQ-GLYTMEHVSGNLYNFLRTRGRALVNTAQLOQFSLHVABG 344
 Db ||:|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 247 NLVQQLGTVEEKGGLYIVTEYMAKGSLSYDYLRSRGSVLLGDCLLKFSLDVCEA 306

QY 345 SKKLVHRRDLAARNLVSLEDVAKYSDFGJAKAERKGQLDSRLPKWTBALKIGKESK 404
 |||||||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
 US-08-701-191A-35
 Sequence 35, Application US/08701191A
 Patent No. 5942428

GENERAL INFORMATION:
 APPLICANT: Mosa Mohammad, Joseph Schlessinger,
 APPLICANT: and Steven R. Hubbard

TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN RECEPTOR TYROSINE KINASE
 NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08701191A
 FILING DATE: August 21, 1996
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 227/088

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-701-191A-35

Query Match 29 8%; Score 797; DB 2; Length 269;
 Best Local Similarity 58.7%; Pred. No. 4.1e-60; Indels 59; Gaps 1;
 Matches 152; Conservative 46; Mismatches 46; Delins 2; Gaps 1;

QY 222 ELARGWLNLNQHLTIGAQIGEGERGAQVLOGEYQGQKAVKNKICDVQAQAFDETAVMT 281
 Db. 1 EFYRGWALMKELKLQQTGKGERGQDMVGDYQNGKNAVKCINKDQAFQAEASVYMLRIS 60

QY 282 KMQRHENLVLRLGVLHQ-GLYTMEHVSGNLYNFLRTRGRALVNTAQLOQFSLHVABG 339
 Db. 61 QLRHNSNLVQQLGTVEEKGGLYIVTEYMAKGSLSYDYLRSRGSVLLGDCLLKFSLDVCEA 120

QY 340 MEYLSKKLVHRRDLAARNLVSLEDVAKYSDFGJAKAERKGQLDSRLPKWTBALKIGKESK 399

RESULT 15
 US-09-035-706-3
 Sequence 3, Application US/09035706
 Patent No. 6001622
 GENERAL INFORMATION:
 APPLICANT: Dechar, Shoukat
 APPLICANT: Hannigan, Greg
 TITLE OF INVENTION: Integrin-Linked Kinase and
 TITLE OF INVENTION: its Uses
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bozzicewic & Reed, LLP
 STREET: 285 Hamilton Avenue, Suite 200
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94301
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEE for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,706
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela J
 REGISTRATION NUMBER: 36,677
 REFERENCE/DOCKET NUMBER: KN-2C1P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-327-3400
 TELEFAX: 650 327-3231
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 258 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-035-706-3

QY 409 SFGVILWEVFSYGRAPPKMSIKESEAVERGYRMEPEGGPGPVHLIMSSCWEAARR 468
 |||:||||::||| |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 181 SFGILLWEIYSFGRVYPRIPLKDVPPRVEKGYKMDAPDGCPPAVYEVMMK 240
 QY 469 PPFRKLAEKL 478
 |||: |||: |||:
 Db 241 PSFLQIREQL 250

Search completed: July 29, 2003, 09:52:34
 Job time : 22 secs

Query Match 28.8%; Score 768; DB 3; Length 258;
 Best Local Similarity 58.8%; Pred. No. 1.2e-57;
 Matches 147; Conservative 45; Mismatches 56; Indels 2; Gaps 1;
 QY 231 NIQHLTIGAQTGEGERGAQVAGQYEGYLGQKVAVKNIKCDVTAQFLDETAVMTKMQHENLVR 290
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 1 NMKELKLQQTGKGEFGDMGLDYRGKNAVKCIKNDATAQFLAERSVMTQLRHSNLQ 60
 QY 291 LIGVILHQ - GLYTVAEHWSGNLVFLRTGRLAINTAQILOFSLHVAEGMEYLESKL 348
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 61 LIQGVIVEKGGLYIVTEYMAKSGSLVDRRLRSRGSVLLGDCILKSFDSVCEAMEYLGNE 120
 QY 349 VRDLAARNLVLEDVAKVSDFLGAKAERKGLDSSRLPVKTAPEALKHOKFTSKDW 408
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 121 VRDLAARNLVLEDVAKVSDFLGAKAERKGLDSSRLPVKTAPEALKHOKFTSKDW 180

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XX
PA (ASAHI) ASAHI KASEI KOGYO KK.
XX
PT Sakano S;
XX
DR WPI; 1995-106842/74.
XX
N-PSDB; AAQ84888.
PT Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy
XX
PS Claim 1; Page 42-44; 58pp; English.
XX
CC A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human U9-7 blood cell line. The DNA sequences and antibodies raised against the enzyme, are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
Sequence 507 AA:
Query Match 100.0%; Score 2671; DB 16; Length 507;
Best Local Similarity 100.0%; Pred. No. 8 6e-242; Mismatches 0; Indels 0; Gaps 0;
Matches 507; Conservative 0; PT
CC 1 MAGRGSLSVWRAFGCDSAEELPVSPLRSRPLRAHPPVSPARMTRWRAPGTOCTKCHT 60
Db 1 MAGRGSLSVWRAFGCDSAEELPVSPLRSRPLRAHPPVSPARMTRWRAPGTOCTKCHT 60
CC 61 RPKGELAERKGKVDTILACENKSWSYRKHHTSGQEGILAGALRERALSADPKLIM 120
Db 61 RPKGELAERKGKVDTILACENKSWSYRKHHTSGQEGILAGALRERALSADPKLIM 120
CC 121 PWFHGKISQEAQVQLQPFPEDGLFLVRESRARHPDGYVLCVSGFGRDVIVHYRVLHRDHGHTI 180
Db 121 PWFHGKISQEAQVQLQPFPEDGLFLVRESRARHPDGYVLCVSGFGRDVIVHYRVLHRDHGHTI 180
CC 181 DEAVFCNCNLMMDVHYSKRGAICTKLVPKRKGTKSAEELARAGWLNLQHLTGQ 240
Db 181 DEAVFCNCNLMMDVHYSKRGAICTKLVPKRKGTKSAEELARAGWLNLQHLTGQ 240
CC 241 IGEGEFGAVLQGEYLQGOKVAVKNIKCDVTAQAFLEDETAVTMKHOHENLVRLGVLHOGI 300
Db 241 IGEGEFGAVLQGEYLQGOKVAVKNIKCDVTAQAFLEDETAVTMKHOHENLVRLGVLHOGI 300
CC 301 YIVMEHVSQGNLYNFLRTRGRALVNTAQILOFSLHVAGMMEYLESKKLVHDLARNILV 360
Db 301 YIVMEHVSQGNLYNFLRTRGRALVNTAQILOFSLHVAGMMEYLESKKLVHDLARNILV 360
CC 361 SEDIWKVSDFGGLAKAERKGKDSSRLPVWTAPALKKGFTKSDWNSFGVLLWEVFSY 420
Db 361 SEDIWKVSDFGGLAKAERKGKDSSRLPVWTAPALKKGFTKSDWNSFGVLLWEVFSY 420
CC 421 GRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVPHMLSSCWAEPPRPFKLAKLAR 480
Db 421 GRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVPHMLSSCWAEPPRPFKLAKLAR 480
CC 481 ELSAGAPASVSGDADGSTSPSQEP 507
Db 481 ELSAGAPASVSGDADGSTSPSQEP 507
RESULT 2
AAQ15860
ID AAQ15860 standard; Protein; 507 AA.
XX
AC AAQ15860;
XX
DT 02-JAN-2003 (first entry)
XX
DE Human matk-related protein.

XX
PA Human; allergic disease; matk gene; atopic dermatitis.
XX
KW
XX
OS Homo sapiens.
XX
PN WO200275304-A1.
XX
PD 26-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-JP01916.
XX
PR 21-MAR-2001; 2001JP-0081028.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
PI Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
DR WPI; 2002-750572/81.
DR N-PSDB; AAL50631.
XX
PT Examining allergic diseases by changes in expression level of matk gene in peripheral monocytes as indication, also applicable in screening compounds for treating allergic diseases e.g. atopic dermatitis.
XX
PS Disclosure; Page 52-55; 60pp; Japanese.
XX
The invention comprises a method of examining allergic diseases, the method comprising comparing the expression level of the matk gene in a biological sample of a patient and a healthy individual. The method of the invention is useful for examining/diagnosing allergic diseases - particularly atopic dermatitis, the method of the invention is also useful in screening candidate compounds for remedies. The present amino acid sequence represents a human matk-related protein.
XX
Sequence 507 AA:
Query Match 100.0%; Score 2671; DB 23; Length 507;
Best Local Similarity 100.0%; Pred. No. 8 6e-242; Mismatches 0; Indels 0; Gaps 0;
Matches 507; Conservative 0; PT
CC 1 MAGRGSLSVWRAFGCDSAEELPVSPLRSRPLRAHPPVSPARMTRWRAPGTOCTKCHT 60
Db 1 MAGRGSLSVWRAFGCDSAEELPVSPLRSRPLRAHPPVSPARMTRWRAPGTOCTKCHT 60
CC 61 RPKGELAERKGKVDTILACENKSWSYRKHHTSGQEGILAGALRERALSADPKLIM 120
Db 61 RPKGELAERKGKVDTILACENKSWSYRKHHTSGQEGILAGALRERALSADPKLIM 120
CC 121 PWFHGKISQEAQVQLQPFPEDGLFLVRESRARHPDGYVLCVSGFGRDVIVHYRVLHRDHGHTI 180
Db 121 PWFHGKISQEAQVQLQPFPEDGLFLVRESRARHPDGYVLCVSGFGRDVIVHYRVLHRDHGHTI 180
CC 181 DEAVFCNCNLMMDVHYSKRGAICTKLVPKRKGTKSAEELARAGWLNLQHLTGQ 240
Db 181 DEAVFCNCNLMMDVHYSKRGAICTKLVPKRKGTKSAEELARAGWLNLQHLTGQ 240
CC 241 IGEGEFGAVLQGEYLQGOKVAVKNIKCDVTAQAFLEDETAVTMKHOHENLVRLGVLHOGI 300
Db 241 IGEGEFGAVLQGEYLQGOKVAVKNIKCDVTAQAFLEDETAVTMKHOHENLVRLGVLHOGI 300
CC 301 YIVMEHVSQGNLYNFLRTRGRALVNTAQILOFSLHVAGMMEYLESKKLVHDLARNILV 360
Db 301 YIVMEHVSQGNLYNFLRTRGRALVNTAQILOFSLHVAGMMEYLESKKLVHDLARNILV 360
CC 361 SEDIWKVSDFGGLAKAERKGKDSSRLPVWTAPALKKGFTKSDWNSFGVLLWEVFSY 420
Db 361 SEDIWKVSDFGGLAKAERKGKDSSRLPVWTAPALKKGFTKSDWNSFGVLLWEVFSY 420
CC 421 GRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVPHMLSSCWAEPPRPFKLAKLAR 480
Db 421 GRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVPHMLSSCWAEPPRPFKLAKLAR 480
CC 481 ELSAGAPASVSGDADGSTSPSQEP 507
Db 481 ELSAGAPASVSGDADGSTSPSQEP 507

QY 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507
 ID AAR84181 standard; Protein: 507 AA.
 Db 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507

RESULT 3
 AAR84181
 ID AAR84181 standard; Protein: 507 AA.
 AC AAR84181;
 XX
 DT 26-MAR-1996 (first entry)
 XX DE . Megakaryocyte kinase MKK1.
 KW Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
 cellular signal transduction; leukaemia; thrombocytopenia.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FT Domain 48..111 /label= SH3_domain
 FT Domain 122..196 /label= SH2_domain
 FT Domain 233..478 /label= Catalytic_domain
 PN W09529185-A1.
 XX PD 02-NOV-1995.
 XX PP 24-APR-1995; 95WO-US05008.
 XX PR 21-APR-1995; 95US-0426509.
 PR 22-APR-1994; 94US-023245.
 XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX (SUGE-) SUGEN INC.
 PT Gishizky M, Sures I, Ullrich A;
 XX WPI; 1995-382959/49.
 DR N-PSDB; AAT00616.
 XX
 PT New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) - used to develop prods. for the treatment and diagnosis of kinase related signal transduction abnormalities.
 XX
 PS Claim 15; Fig 1A-C; 82pp; English.
 XX
 CC Human megakaryocyte kinase MKK1 (AAR84181) is a 58 kDa cytosolic tyrosine kinase showing 54% homology with csk. It appears to play a regulatory role in the growth and differentiation of megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be produced in host cells by expression of encoding cDNA (AAT00616), and used in the treatment and diagnosis of e.g. leukaemia and thrombocytopenia.
 XX
 SQ Sequence 507 AA;

Query Match 99.9%; Score 2668; DB 16; Length 507;
 Best Local Similarity 99.8%; Pred. No. 1.6e-241;
 Matches 506; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGRSIVSWRAFHGCDSAEELPRVSPRFRLRAWHPPVSARMPTTRWAPGTOCITKCEHT 60
 1 MAGRGSIVSWRAFHGCDSAEELPRVSPRFRLRAWHPPVSARMPTTRWAPGTOCITKCEHT 60
 Db 61 RPKPGELAFRKDVVTLIEACENKSWRKHHTSGDGGLLAGALREREALSDPKLSM 120
 QY 61 RPKPGELAFRKDVVTLIEACENKSWRKHHTSGDGGLLAGALREREALSDPKLSM 120

QY 121 PWHGKLSQEAQVQLQOPPEDGLFLVRSARHGDYVLCVSFRGRDVHYVLAHRDHLT 180
 ID AAR71132 standard; Protein: 466 AA.
 Db 121 PWFGKLISQEAQVQLQOPPEDGLFLVRESARHGDYVLCVSFRGRDVHYVLRDHLT 180

QY 181 DEAVFFCNLMDMVHEHYSKDKGACTTKLVRPKRKHGTSAAEELARAQSWLNQHHTGQ 240
 ID AAR71132 standard; Protein: 466 AA.
 Db 181 DEAVFFCNLMDMVHEHYSKDKGACTTKLVRPKRKHGTSAAEELARAQSWLNQHHTGQ 240

QY 301 YTVMHEVSKGNLYNFLRTRGRALVNTQLOPSLHVAGMELESKVHLRDLARNLV 360
 ID AAR71132 standard; Protein: 466 AA.
 Db 301 YTVMHEVSKGNLYNFLRTRGRALVNTQLOPSLHVAGMELESKVHLRDLARNLV 360

QY 361 SEDLVAKYSDFGLAKAERKGLOSLPVLKWTABEALKHGKFPSKSDWSFGYLWEVFSY 420
 ID AAR71132 standard; Protein: 466 AA.
 Db 361 SEDLVAKYSDFGLAKAERKGLOSLPVLKWTABEALKHGKFPSKSDWSFGYLWEVFSY 420

QY 421 GRAFPYKMSIKEYSEAVKGYMPPECGCPGVPHLSSCWEAPARRPFKLAELAR 480
 ID AAR71132 standard; Protein: 466 AA.
 Db 421 GRAFPYKMSIKEYSEAVKGYMPPECGCPGVPHLSSCWEAPARRPFKLAELAR 480

QY 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507
 ID AAR84181 standard; Protein: 507 AA.
 Db 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507

RESULT 4
 AAR71132
 ID AAR71132 standard; Protein: 466 AA.
 AC AAR71132;
 XX DT 25-MAR-2003 (updated)
 XX DT 27-OCT-1995 (first entry)
 DE N-terminal truncated cytoplasmic tyrosine kinase.
 XX KW cytoplasmic; tyrosine kinase; blood; cell differentiation; screening; anticancer agent; SH3; src homology domain.
 XX OS Homo sapiens.
 XX
 Key Location/qualifiers
 FT Domain 7..70 /note= "SH3 domain"
 FT Domain 81..155 /note= "SH2 domain"
 FT Domain 192..438 /note= "tyrosine kinase domain"
 PN W09506113-A1.
 XX PD 02-MAR-1995.
 XX PF 25-AUG-1994; 94WO-JP01411.
 XX PR 25-AUG-1993; 93JP-0210403.
 PR 29-MAR-1994; 94JP-0058553.
 XX PA (ASAH) ASAHI KASEI KOGYO KK.
 PI Sakano S;
 XX DR WPI; 1995-106842/14.
 DR N-PSDB; AA084888.

XX Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy

DB	471	...-SANWPRSWPGSYAVQVQPQPSQ	492
RESULT	6		
ID	AAU9575	AAU9575 standard; Protein; 415 AA.	
ID	AAU9575	AAU9575;	
XX	XX	21-OCT-2002 (first entry)	
XX	XX	Human kinase related to tyrosine kinase family.	
KW	KW	Human; kinase; tyrosine kinase; kinase mediated disorder; haematopoietic disorder; cell signal transduction disorder; cancer; haemostatic; cytostatic; enzyme.	
XX	XX	Homo sapiens.	
OS	XX	PN WO20252018-A2.	QY 302 TMEHVRGNGNLVAFRLTRGRALNTAQIQLQFSHLVAEGNEYLESKKLVIRDLARNLVS 361
XX	XX	PD 04-JUL-2002.	Db 210 TMEHVKSGNLVFLTRGRALNTAQIQLQFSHLVAEGNEYLESKKLVIRDLARNLVS 269
XX	XX	PF 19-DEC-2001; 2001WO-US48546.	AC AAR71131; QY 362 EDLVAKVSDFGLAKAERKGDDSSRLPVKWTPEALKHGKFTTSKSDWVPGVLLMVEFSYG 421
XX	XX	PR 21-DEC-2000; 2000US-0741154.	Db 270 EDLVAKVSDFGLAKAERKGDDSSRLPVKWTPEALKHGKFTTSKSDWVPGVLLMVEFSYG 329
PA	(PEKE) PE CORP NY.	PA Beasley EM, Shao W, Ketchum K, Di Francesco V, DR N-PSDB; ABK88791, ABK88792.	QY 422 RAPYKMSLKESEAVERGYRMRMPPGEGCPGVHLMSSCWEAPPARRPPFKLAELARE 481
XX	XX	PI XX WPI; 2002-583568/62.	Db 330 RAPYKMSLKESEAVERGYRMRMPPGEGCPGVHLMSSCWEAPPARRPPFKLAELARE 389
PS	XX	DR 2000US-0741154.	QY 482 LRSAGAPASVSGDADGSTSPRQEP 507
XX	XX	PT (PEKE) PE CORP NY.	Db 390 LRSAGAPASVSGDADGSTSPRQEP 415
XX	XX	PT PI Beasley EM, Shao W, Ketchum K, Di Francesco V, DR N-PSDB; ABK88791, ABK88792.	RESULT 7
XX	XX	PT PR 21-DEC-2000; 2000US-0741154.	AAR71131 AAR71131 standard; Protein; 246 AA.
XX	XX	PT PA (PEKE) PE CORP NY.	XX AAR71131;
XX	XX	PT XX WPI; 2002-583568/62.	XX AAR71131; DT 25-MAR-2003 (updated)
XX	XX	PT DR 2000US-0741154.	XX 27-OCT-1995 (first entry)
XX	XX	PT PA 21-DEC-2000; 2000US-0741154.	DE Tyrosine kinase domain of cytoplasmic tyrosine kinase.
XX	XX	PT PR PA (PEKE) PE CORP NY.	XX cytoplasmic; tyrosine kinase; blood; cell differentiation; KW screening; anticancer agent.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX screening; anticancer agent.
XX	XX	PT PR XX WPI; 2002-583568/62.	OS Homo sapiens.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX OS Homo sapiens.
XX	XX	PT PR XX WPI; 2002-583568/62.	PN WO9506113-A1.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX 02-MAR-1995.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX 25-AUG-1994; 94WO-JP01411.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX 25-AUG-1994; 93JP-0210403.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX 29-MAR-1994; 94JP-005853.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX PA (ASAHI ASAKI KASEI KOGYO KK).
XX	XX	PT PR XX WPI; 2002-583568/62.	XX PI Sakano S;
XX	XX	PT PR XX WPI; 2002-583568/62.	XX DR WPI; 1995-106842/14.
XX	XX	PT PR XX WPI; 2002-583568/62.	DR N-PSDB; AAB64888.
XX	XX	PT PR XX WPI; 2002-583568/62.	Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy
XX	XX	PT PR XX WPI; 2002-583568/62.	XX PS Claim 1; Page 39; 58pp; English.
XX	XX	PT PR XX WPI; 2002-583568/62.	XX CC A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human UT-7 blood cell line. This sequence comprises the tyrosine kinase domain of the enzyme (residues 192-437 of AAR71132; residues 233-478 of AAR71133). The DNA sequences and antibodies raised against the enzyme are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. (Updated on 25-MAR-2003 to correct PN field.)
XX	XX	PT PR XX WPI; 2002-583568/62.	XX Sequence 246 AA;
QY	QY	Query Match Best Local Similarity 75.3%; Score 2012; DB 23; Length 415; Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human UT-7 blood cell line. This sequence comprises the tyrosine kinase domain of the enzyme (residues 192-437 of AAR71132; residues 233-478 of AAR71133). The DNA sequences and antibodies raised against the enzyme are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. (Updated on 25-MAR-2003 to correct PN field.)
Db	Db	Db 90 EAFFCNLMDMVHYSKDKGAICTKLVPRKRKHGTSAEELARGWLNLQHITLGAQI 149	CC Query Match Best Local Similarity 47.2%; Score 1261; DB 16; Length 246; Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	Db	Db 242 GEGERFAGVILQGETIGQKAVKNIKCDVYQAFLDETAVMTKMOHENLVRLVLRGIVHOLY 301	CC QY 233 QHITLGAQIGEGERFAGVILQGETIGQKAVKNIKCDVYQAFLDETAVMTKMOHENLVRLVLRGIVHOLY 292
Db	Db	Db 150 GEGERFAGVILQGETIGQKAVKNIKCDVYQAFLDETAVMTKMOHENLVRLVLRGIVHOLY 209	CC QHITLGAQIGEGERFAGVILQGETIGQKAVKNIKCDVYQAFLDETAVMTKMOHENLVRLVLRGIVHOLY 292

	SQ	Sequence	459 AA;
Db	1	QHLTGQAQGEGECAVLOGEYLGKQKVAKNIKQDVTAAFLDETAWMKMOHENLVRRL 60	
Qy	293	GVLHOGLYTMEHVSKGNLVNFLRURGRLVNTQOLLSFLHVAGEMEYLESKKLVHRD 352	
Db	61	GVLHOGLYTMEHVSKGNLVNFLRURGRLVNTQOLLSFLHVAGEMEYLESKKLVHRD 120	
Qy	353	LAARNITLVESDLVAKVSDGLAKAERKGKDLSRSLVWPAPEALKHGKPTSKSYWSFGV 412	
Db	121	LAARNITLVESDLVAKVSDGLAKAERKGKDLSRSLVWPAPEALKHGKPTSKSYWSFGV 180	
Qy	413	LLWEFSYGRAPYKPKMSLKEVEAVKGRMPEPGCPGVHVLMSCCWAEAPRRPPR 472	
Db	181	LLWEFSYGRAPYKPKMSLKEVEAVKGRMPEPGCPGVHVLMSCCWAEAPRRPPR 240	
Qy	473	KLAEKL 478	
Db	241	KLAEKL 246	
RESULT 8			
AA013873			
ID	AA013873 standard; Protein; 459 AA.		
AC	AA013873;		
XX			
XX			
DT	06-Nov-2001 (first entry)		
XX			
DE	Human polypeptide SEQ ID NO 27765.		
XX			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulator; cancer; leukaemia; nervous system disorders; arthritis; inflammation.		
KW	Homo sapiens.		
XX			
PN	WO200164835-A2.		
XX			
PD	07-SEP-2001.		
XX			
PF	26-FEB-2001; 2001WO-US04927.		
XX			
PR	28-FEB-2000; 2000US-0515126.		
PR	18-MAY-2000; 2000US-0577409.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PT	Tang YT, Liu C, Drmanac RT;		
XX			
DR	WPI; 2001-514838/56.		
DR	N-PSDB; AA193804.		
PT	Isolated nucleic acids and polypeptides, useful for preventing PT diagnosing and treating e.g. leukaemia, inflammation and immune disorders.		
XX			
PS	Claim 20; SEQ ID NO 27765; 1399pp + Sequence Listing; English.		
XX			
CC	The invention relates to human polynucleotides (AAI7941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity relating to production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibit activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.		
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .		
XX			
RESULT 9			
AAV4448			
ID	AAV4448 standard; Protein; 450 AA.		
XX			
AC	AAV4448;		
XX			
DT	22-MAR-2000 (first entry)		
XX			
DE	Wild-type human c-Src tyrosine kinase.		
XX			
KW	Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate; human; viral expression vector; replication competent; mutant Src; inflammatory disease; arthritis; rheumatoid arthritis; restenosis; diabetic retinopathy; osteoporosis; cancer.		
XX			
PT	Homo sapiens.		
OS			
XX			
PN	WO951590-A1.		
XX			
PD	02-DEC-1999.		
XX			
PF	28-MAY-1999; 99WO-US11780.		
XX			
PR	29-MAY-1998; 98US-0087220.		
XX			
PA	(SCRI) SCRIPPS RES INST.		
XX			
PI	Cheresh DA, Elceirri B, Schwartzberg PL;		
XX			
DR	WPI; 2000-116335/10.		
DR	N-PSDB; AAZ29701.		
XX			
PT	Using tyrosine kinase Src for modulating angiogenesis in tissues useful in, e.g. treatment of chronic articular rheumatism -		

PS	Claim 1; Fig 4; 80pp; English.
XX	The present sequence is the wild-type human c-Src tyrosine kinase. This
CC	Src protein can be used to modulate angiogenesis. When the Src protein
CC	is inactivated, angiogenesis is inhibited, while when it is activated,
CC	angiogenesis is potentiated. The modified or variant Src can be used to
CC	treat inflammatory diseases like, arthritis, rheumatoid arthritis,
CC	diabetic retinopathy, restenosis, osteoporosis and cancer associated
CC	disorders.
SQ	Sequence 450 AA;
Qy	Query Match 46.6%; Score 1245.5; DB 21; Length 450;
Db	Best Local Similarity 54.1%; Pred. No. 5.5e-108; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
Qy	47 WAPGTOCITKCEHTRPKPGEALAFRKGDVWTLIEACENKSWWRVKHHQSQEGGLAAGALR 106
Db	8 WPSGTECIANKNFHGTAQFDQPLPKGDLVTLAVKDPNWAKKVV-GREGIIPANYVQ 66
Qy	107 EREALASADPKSLIMPWFHGKISQEAQVOOLQPPEGLFLVRESEARHPGDYVILCVSFRDV 166
Db	67 KREGVKAGTKLSSLMPWFHGKTRREQEQLLPETGLFLVRESTNYPGDYVILCVSCDGV 126
Qy	167 IHRVLRDGHLTIDEAVFFCNLMQDVMEHYSKPGKACTKLVRPKRKGTKSAEELARA 226
Db	127 EHYRIMTHASKLSIDEEVFENLQMOLVEHYTSADGLCTRLIKPKMECTVAQDEFYRS 186
Qy	227 GWLNLTQHLTGAQIGGEGFAGVQLGEVLGQKAVKNAKICDVTQAQFLDETAVMKHOE 286
Db	187 GWAHLNKKELKLQIOTKGKGEFDGMGLDGRKAVKCIKNDATAQFLAEASYMTQLRS 246
Qy	287 NUVLRLGVLHQ--GYIYMHVHSKGKGNLNFRLTRGRALVNTAQLOFLSLHVAGEMYLE 344
Db	247 NLVOLLGIVTEERGGLYIVTEYMAKGSGLVDYLRSGRSVLGDCILKESDVCMEAYLE 306
Qy	345 SKKLVRDLDARNILVSDLVAKVSDFGLKAFAERKGKGLDSSRLPVKWTAPEALKHGKFSTK 404
Db	307 GNNFYHRLAARNVLVNLVSEDNVAKVSDFGLTKEASSTQDTGKLVKWTAPEALKERKFSTK 366
Qy	405 SDWWSFGVLLWEVFSYGRAPYKPMKSLKEVSEAEVKGYRMEEPPGCCPGPVHVLMSSCWRE 464
Db	367 SDWWSFGVLLWEVFSYGRAPYKPIPLKDVPVREVKYMDAPDGCPAPPAYEVMKNCWHL 426
Qy	465 PARRPFKRKLAEKI 478
Db	427 AAMRPSFLQLRQEL 440
RESULT 10	
AY49418	ID AY49418 standard; Protein; 450 AA.
XX	DT 13-MAR-2000 (first entry)
AC	AY49418;
XX	DE PKA substrate, Csk-family protein.
XX	KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer; kinase substrate; immunosuppressive disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease; Chk; Lsk; Hyl; systemic lupus erythematosus; Csk-family; Matk; Ctk; Btk; Ntk.
OS Homo sapiens.	
XX	PN W09962315-A2.
XX	PD 02-DEC-1999.
XX	PP 27-MAY-1999; 99WO-GB01680.
PR	27-MAY-1998; 98NO-000419.
PR	30-DEC-1998; 98US-0114240.
PA	(LAUR-) LAURAS AS.
PA	(JONE/) JONES E. L.
PI	Hansson V, Levy FO, Mustelin T, Skalnegg BS, Sundvold V, Tasken K;
PI	Vang T, Altman A, Munshi A;
XX	DR WPI; 2000-086801/07.
DR	N-PSDB; AAZ46489.
XX	PT Altering the activity of protein kinase signaling pathways, used for treating immunosuppressive disorders, e.g. AIDS, proliferative disorders, e.g. cancers or autoimmune diseases
PS	Claim 12; Page 89-90; 11pp; English.
XX	The invention provides a novel method of altering the activity of the protein kinase A (PKA) signaling pathway in a cell that comprises altering the extent of phosphorylation or one or more PKA substrates, or kinase substrates downstream in the PKA signaling pathway. Pharmaceutical compositions containing a nucleic acid molecule that encodes a PKA substrate or fragment, precursor or functionally equivalent variant, where the sequence is modified to alter its susceptibility to phosphorylation by PKA can be used for treating a disorder exhibiting abnormal PKA signaling activity. Immunosuppressive disorders or proliferative diseases. They can be used for treating e.g. HIV infection, AIDS, common variable immunodeficiency or cancers. Conditions in which upregulation of the PKA pathway is required, such as autoimmune disease, e.g. systemic lupus erythematosus, may also be treated. The present sequence represents a PKA substrate, wherein the substrate is in the Csk-family, preferably Csk, Chk, Lsk, Hyl, Matk, Ctk, Btk or Ntk.
SQ	Sequence 450 AA;
Qy	Query Match 46.6%; Score 1245.5; DB 21; Length 450;
Db	Best Local Similarity 54.1%; Pred. No. 5.5e-108; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
Qy	47 WAPGTOCITKCEHTRPKPGEALAFRKGDVWTLIEACENKSWWRVKHHQSQEGGLAAGALR 106
Db	8 WPSGTECIANKNFHGTAQFDQPLPKGDLVTLAVKDPNWAKKVV-GREGIIPANYVQ 66
Qy	107 EREALASADPKSLIMPWFHGKISQEAQVOOLQPPEGLFLVRESEARHPGDYVILCVSFRDV 166
Db	67 KREGVKAGTKLSSLMPWFHGKTRREQEQLLPETGLFLVRESTNYPGDYVILCVSCDGV 126
Qy	167 IHRVLRDGHLTIDEAVFFCNLMQDVMEHYSKPGKACTKLVRPKRKGTKSAEELARA 226
Db	127 EHYRIMTHASKLSIDEEVFENLQMOLVEHYTSADGLCTRLIKPKMECTVAQDEFYRS 186
Qy	227 GWLNLTQHLTGAQIGGEGFAGVQLGEVLGQKAVKNAKICDVTQAQFLDETAVMKHOE 286
Db	187 GWAHLNKKELKLQIOTKGKGEFDGMGLDGRKAVKCIKNDATAQFLAEASYMTQLRS 246
Qy	287 NUVLRLGVLHQ--GYIYMHVHSKGKGNLNFRLTRGRALVNTAQLOFLSLHVAGEMYLE 344
Db	247 NLVOLLGIVTEERGGLYIVTEYMAKGSGLVDYLRSGRSVLGDCILKESDVCMEAYLE 306
Qy	345 SKKLVRDLDARNILVSDLVAKVSDFGLKAFAERKGKGLDSSRLPVKWTAPEALKHGKFSTK 404
Db	307 GNNFYHRLAARNVLVNLVSEDNVAKVSDFGLTKEASSTQDTGKLVKWTAPEALKERKFSTK 366
Qy	405 SDWWSFGVLLWEVFSYGRAPYKPMKSLKEVSEAEVKGYRMEEPPGCCPGPVHVLMSSCWRE 464
Db	367 SDWWSFGVLLWEVFSYGRAPYKPIPLKDVPVREVKYMDAPDGCPAPPAYEVMKNCWHL 426
Qy	465 PARRPFKRKLAEKI 478
Db	427 AAMRPSFLQLRQEL 440

RESULT 11
 Db AAB84662 ID AAB84662 standard; Protein: 450 AA.
 XX AC AAB84662;
 XX DT 05-SEP-2001 (first entry)
 DE Amino acid sequence of human tyrosine kinase protein Src.
 XX
 KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke; diabetic retinopathy; inflammatory disease; infection; arthritis; adult respiratory distress syndrome; ARDS; rheumatoid arthritis; capillary proliferation; psoriasis; neovascular glaucoma; XX OS Homo sapiens.
 XX WO200145751-A1.
 PR 29-MAR-2000; 2000US-0538248.
 PD 28-JUN-2001.
 XX PF 22-DEC-2000; 2000WO-US35396.
 PR 22-DEC-1999; 99US-0470881.
 PR 29-MAR-2000; 2000US-0538248.
 PA (SCRI) SCRIPPS RBS INST.
 XX PT Chareesh DA, Elieceiri B, Paul R;
 XX DR WPI; 2001-417982/44.
 DR N-PSDB; AAH28358.
 XX PT Modulating vascular permeability in tissues, including inflamed tissue, tissues associated with stroke, myocardial infarction, by contacting the tissue with tyrosine kinase protein Src, Yes or their modified forms -
 XX PS Disclosure; Fig 4; 133pp; English.
 XX The specification describes a method for modulating vascular permeability in a tissue suffering from a disease condition. The method comprises contacting the tissue with a pharmaceutical composition comprising tyrosine kinase protein Src, Yes or their mixtures or nucleic acid expressing them. The method is useful for modulating vascular permeability in tissues, including inflamed tissue, tissues associated with stroke, myocardial infarction or other blockage of normal flow, tissues undergoing restenosis, psoriatic, retinal tissue and similar tissues. Pathologies which may be treated include trauma to blood vessels, and other systemic pathological events such as atherosclerosis, diabetic retinopathy, inflammatory disease due to infection by microbial agents and arthritis. Other diseases which can be treated include adult respiratory distress syndrome (ARDS), rheumatoid arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma, capillary proliferation in atherosclerotic plaques and osteoporosis and cancer associated disorders such as solid tumours, solid tumour metastases, angiofibromas and hemangiomas. The present sequence represents human Src, and is used in the method of the invention.
 XX SQ Sequence 450 AA:
 Query Match 46.6%; Score 1245.5; DB 22; Length 450; Best Local Similarity 54.1%; Pred. No. 5.5e-108; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Db 67 KRGVKAGTKLSLMPWPHGKITREQABRLYPPETGFLVRSTNPYGDYLCLVSDGKV 126
 QY 167 IHRVLRHDGHITDEAVFFCNLMDEHYHSKDKGAICTKLVRPKRKHGKSAEELARA 226
 XX 127 EHRIMYHASKLISIDEEVYFENLMOVHEYTSADGLCTRJKPKVMEGTVAQDFYRS 186
 XX
 Db 227 GWLNLNQHILTGQIGGEGFAGVQGLQVAKWNIKCDVTAOFPLDEPAWMTHQE 286
 QY 187 GWALNMBKLLOLTIGKEFGDVMGLGDYQRGNKAVAKCIKNDATAQAFLAESVMTQURHS 246
 Db 287 NLVQLLGVLHQ-GLYVUMEHVSKGNLVNFLETGRALVNTAQLOFSLHVAGEYLE 344
 QY 247 NLVQLLGVLHQ-GLYVUMEHVSKGNLVNFLETGRALVNTAQLOFSLHVAGEYLE 306
 Db 345 SKKLVRHDLAARNLIVSVDLAKVAVSDGLAKERKGKLDSSRLPVKVNTPAELALKHGKPTSK 404
 QY 367 SDWWSFGILLWEIYSFGVPRVYPRIPKDVVPVREKGYRMDADPDCPPAVYEVKWNQHWLD 426
 Db 307 GNVFVHROLAARNLVSDNAVKVSDGLTKEASSTQPTGKLPVKTAAPEALEKKFSTK 366
 PR 405 SDWWSFGILLWEIYSFGVPRVYPRIPKDVVPVREKGYRMDADPDCPPAVYEVKWNQHWLD 464
 PR 367 SDWWSFGILLWEIYSFGVPRVYPRIPKDVVPVREKGYRMDADPDCPPAVYEVKWNQHWLD 426
 PA 465 PARRPPFKLAEKL 478
 Db 427 AAHRPSFLQLREGQ 440

RESULT 12
 ID AAG67444 standard; Protein: 450 AA.
 XX AC AAG67444;
 XX DT 26-NOV-2001 (first entry)
 DE Amino acid sequence of a human polypeptide.
 XX Human; protein kinase; protein phosphatase; signal transduction; KW intracellular signalling pathway.
 XX OS Homo sapiens.
 XX PN WO200109345-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-JP05060.
 XX PR 29-JUL-1999; 99JP-0348036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX DR WPI; 2001-564736/63.

PT New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes -
 XX PS Example 4; Page 249-252; 336pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases. The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to

QY 47 WARSTOCITCKCEHTTRPKPGELAERFKGQYVTLIFACENKSWYRKHNTSGQEGLLAAGALR 106
 DB 8 WPSGTECIAKYNFHGTAEODLPLPKGKDVTIVTAVTKDPNWYKAKNKV-GREGILIPANYVQ 66
 QY 107 EREALSAPKKLSLMPWPHGKISQEAVQQLQPEDGFLVRESARHRCGDDVLCVSFRGDV 166
 :: : | :: : | :: : | :: : | :: : | :: : | :: : | :: : | :: : | :: : | :: : |

CC treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development. The present sequence
 CC represents a polypeptide, used in the course of the invention.
 XX

SQ sequence 450 AA:

Query	Match	Similarity	Score	DB	22;	Length	450;
Best Local				Pred.	No.	5.5e-108;	
Matches	235;	Conservative	81;	Mismatches	115;	Indels	3;
				Gaps	2;		

OY

```
47 WAPGOTCITKEHTRPKGELAFRKGDVYTLEACENKSWKRVKHITSQEGGLAAGALR 106
| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
8 WPSGTECIAKYNFHGTAEQDLIPFCKGDVLTIVAVTKDPNWKAKNKV-GREGITIANYVQ 66
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OY

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107 EREALSADPKISLMPWPHGKTSQEOAVQQLQOPPEDGLFLVRERSARHPGDYVLCVSFRGDV 166
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
67 KREGVAKTKISLMPWPHGKTREOERLIPPERGLFLVRERSARHPGDYVLCVSFRGDV 126
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
167 IYRVLVLRDGHLTIDAEVFFCNLMDMVEHYSKDKGAICTKLVRKRGHTSGEGGLAAGALR 226
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
127 EHRYMHASKLISIDEEVYFFNLMLQVLEHTSDADGICTRILIKPKMEGTVAQDEFYRS 186
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
227 GWLNLNQHLTIGAQIGEGCAGVQIYLGKQVAKNIKVDTQAFDDETAVMKMQE 286
| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
187 GWALNMKELKLIQQTIGKGEFGDVMGLDGYRGKVKAVCIKNDATAQAFLAESVMTQLRHS 246
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
OY


```
287 NUVRLGVLHQ--GLYTIVMEHVSKGNLNUFLTRGRALVTAQLOFSLHVAEGMLE 344
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



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247 NLVOLQGVIVVERKGGIYVTEVMAKSGLVYDYLRSGRSVLGGDCILKFSLVDCEAMEYLE 306
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
345 SKKLVHDLAARNILVSEDLVAKVSDGLAKAERKGKLDDSSLRPLVKWTAPEALKHGKFTSK 404
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
307 GNNFVHDLAARNLVSEDNVAKVSDGLKTRKASSQDTGKLPVKWTAPEALKFKSTK 366
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
405 SDWWSGVLLMVEVFSGRAPYKPKMSLKEVSAEVEKGYMRPEEGCPGPVHLMSSCWEAE 464
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
367 SDWWSFGILLMWIYFSGRVPYPRIPLKDVVPVREKGYKMDAPDGCPPAVIEVMKNCWHLID 426
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
QY


```
465 PARRPPEPKLAEKL 478
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```


OY


```
427 AMRPPSFQIQLRQQL 440
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

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RESULT 13

SQ Sequence 450 AA;

Query	Match	Similarity	Score	DB	22;	Length	450;
Best Local				Pred.	No.	5.5e-108;	
Matches	235;	Conservative	81;	Mismatches	115;	Indels	3;
				Gaps	2;		

OY

```
47 WAPGOTCITKEHTRPKGELAFRKGDVYTLEACENKSWKRVKHITSQEGGLAAGALR 106
| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
8 WPSGTECIAKYNFHGTAEQDLIPFCKGDVLTIVAVTKDPNWKAKNKV-GREGITIANYVQ 66
```

OY

```
107 EREALSADPKISLMPWPHGKTSQEOAVQQLQOPPEDGLFLVRERSARHPGDYVLCVSFRGDV 166
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
67 KREGVAKTKISLMPWPHGKTREOERLIPPERGLFLVRERSARHPGDYVLCVSFRGDV 126
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
167 IYRVLVLRDGHLTIDAEVFFCNLMDMVEHYSKDKGAICTKLVRKRGHTSGEGGLAAGALR 226
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
127 EHRYMHASKLISIDEEVYFFNLMLQVLEHTSDADGICTRILIKPKMEGTVAQDEFYRS 186
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
227 GWLNLNQHLTIGAQIGEGCAGVQIYLGKQVAKNIKVDTQAFDDETAVMKMQE 286
| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
187 GWALNMKELKLIQQTIGKGEFGDVMGLDGYRGKVKAVCIKNDATAQAFLAESVMTQLRHS 246
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
OY


```
287 NUVRLGVLHQ--GLYTIVMEHVSKGNLNUFLTRGRALVTAQLOFSLHVAEGMLE 344
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
307 GNNFVHDLAARNLVSEDNVAKVSDGLKTRKASSQDTGKLPVKWTAPEALKFKSTK 366
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
405 SDWWSGVLLMVEVFSGRAPYKPKMSLKEVSAEVEKGYMRPEEGCPGPVHLMSSCWEAE 464
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
367 SDWWSFGILLMWIYFSGRVPYPRIPLKDVVPVREKGYKMDAPDGCPPAVIEVMKNCWHLID 426
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
QY


```
465 PARRPPEPKLAEKL 478
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```


OY


```
427 AMRPPSFQIQLRQQL 440
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

```


```


```

RESULT 14

SQ Sequence 450 AA;

Query	Match	Similarity	Score	DB	22;	Length	450;
Best Local				Pred.	No.	5.5e-108;	
Matches	235;	Conservative	81;	Mismatches	115;	Indels	3;
				Gaps	2;		

OY

```
345 SKKLVHDLAARNILVSEDLVAKVSDGLAKAERKGKLDDSSLRPLVKWTAPEALKHGKFTSK 404
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```

OY

```
307 GNNFVHDLAARNLVSEDNVAKVSDGLKTRKASSQDTGKLPVKWTAPEALKFKSTK 366
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
405 SDWWSGVLLMVEVFSGRAPYKPKMSLKEVSAEVEKGYMRPEEGCPGPVHLMSSCWEAE 464
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```

OY

```
367 SDWWSFGILLMWIYFSGRVPYPRIPLKDVVPVREKGYKMDAPDGCPPAVIEVMKNCWHLID 426
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
QY


```
465 PARRPPEPKLAEKL 478
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
427 AMRPPSFQIQLRQQL 440
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

```


```

PI Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.;
 PI Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Funahashi, S.;
 PI Seno, C., Nezu, J.;
 XX

DR. WPI; 2001-570286/64.

PT New genes encoding proteins with protein kinase/protein phosphatase

PT activity, useful in the diagnosis and treatment of diseases -

PT Example 4; Page 149-152; 233pp; Japanese.

The specification describes human protein kinase/protein phosphatases. It is expected that the protein kinase/protein phosphatase gene participates in signal transduction in cells. The protein kinase/protein phosphatase polypeptides and polynucleotides are useful for developing diagnostics and treatment agents for human and animal diseases. The protein kinase/protein phosphatase polypeptides are useful as target molecules in designing novel drugs. The protein kinase/protein phosphatase polynucleotides are useful as a source of probes and primers, which may be used to isolate homologous sequences. The present sequence represents a human protein, which is used in the course of the invention.

RESULT 15

SQ Sequence 450 AA;

Query	Match	Similarity	Score	DB	22;	Length	450;
Best Local				Pred.	No.	5.5e-108;	
Matches	235;	Conservative	81;	Mismatches	115;	Indels	3;
				Gaps	2;		

OY

```
47 WAPGOTCITKEHTRPKGELAFRKGDVYTLEACENKSWKRVKHITSQEGGLAAGALR 106
| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
8 WPSGTECIAKYNFHGTAEQDLIPFCKGDVLTIVAVTKDPNWKAKNKV-GREGITIANYVQ 66
```

OY

```
107 EREALSADPKISLMPWPHGKTSQEOAVQQLQOPPEDGLFLVRERSARHPGDYVLCVSFRGDV 166
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
67 KREGVAKTKISLMPWPHGKTREOERLIPPERGLFLVRERSARHPGDYVLCVSFRGDV 126
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
167 IYRVLVLRDGHLTIDAEVFFCNLMDMVEHYSKDKGAICTKLVRKRGHTSGEGGLAAGALR 226
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
127 EHRYMHASKLISIDEEVYFFNLMLQVLEHTSDADGICTRILIKPKMEGTVAQDEFYRS 186
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
227 GWLNLNQHLTIGAQIGEGCAGVQIYLGKQVAKNIKVDTQAFDDETAVMKMQE 286
| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
187 GWALNMKELKLIQQTIGKGEFGDVMGLDGYRGKVKAVCIKNDATAQAFLAESVMTQLRHS 246
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
OY


```
287 NUVRLGVLHQ--GLYTIVMEHVSKGNLNUFLTRGRALVTAQLOFSLHVAEGMLE 344
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
307 GNNFVHDLAARNLVSEDNVAKVSDGLKTRKASSQDTGKLPVKWTAPEALKFKSTK 366
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
405 SDWWSGVLLMVEVFSGRAPYKPKMSLKEVSAEVEKGYMRPEEGCPGPVHLMSSCWEAE 464
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
367 SDWWSFGILLMWIYFSGRVPYPRIPLKDVVPVREKGYKMDAPDGCPPAVIEVMKNCWHLID 426
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
QY


```
465 PARRPPEPKLAEKL 478
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```


OY


```
427 AMRPPSFQIQLRQQL 440
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

```


```


```

RESULT 16

SQ Sequence 450 AA;

Query	Match	Similarity	Score	DB	22;	Length	450;
Best Local				Pred.	No.	5.5e-108;	
Matches	235;	Conservative	81;	Mismatches	115;	Indels	3;
				Gaps	2;		

OY

```
345 SKKLVHDLAARNILVSEDLVAKVSDGLAKAERKGKLDDSSLRPLVKWTAPEALKHGKFTSK 404
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```

OY

```
307 GNNFVHDLAARNLVSEDNVAKVSDGLKTRKASSQDTGKLPVKWTAPEALKFKSTK 366
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
405 SDWWSGVLLMVEVFSGRAPYKPKMSLKEVSAEVEKGYMRPEEGCPGPVHLMSSCWEAE 464
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```

OY

```
367 SDWWSFGILLMWIYFSGRVPYPRIPLKDVVPVREKGYKMDAPDGCPPAVIEVMKNCWHLID 426
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
QY


```
465 PARRPPEPKLAEKL 478
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db
```



OY



```
427 AMRPPSFQIQLRQQL 440
:||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

```


```

XX Human; breast cancer; cytostatic; gene therapy.

XX Homo sapiens.
 OS WO2003004989-A2.
 XX PD 16-JAN-2003.
 XX PR 21-JUN-2002; 2002WO-US19669.
 XX PR 21-JUN-2001; 2001US-299887P.
 PR 27-JUN-2001; 2001US-301572P.
 PR 18-JUL-2001; 2001US-300501P.
 PR 25-SEP-2001; 2001US-325002P.
 PR 05-MAR-2002; 2002US-362585P.
 PR 14-MAY-2002; 2002US-380391P.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S, Mertens M;
 PI Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE, Bast RC;
 PI Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
 XX WPI: 2003-210381/20.
 DR N-SSDB; ACC50120.

XX PT Breast cancer diagnosis or treatment by comparing the level of
 PT expression of a marker in a patient sample with that in the control
 PT non-breast cancer sample -
 XX PS Claim 1: SEQ ID 88; 128pp; English.

CC The present invention describes a method for assessing whether a patient
 CC is afflicted with breast cancer. The method comprises comparing the level
 CC of expression of a marker (gene/polypeptide see ACC50076 to ACC5034 and
 ABR7386 to ABR7332) in a patient sample and the normal level of
 CC expression of the marker in a control non-breast cancer sample, where a
 CC significant increase in the level of expression of the marker in the
 CC patient sample and the normal level is an indication that the patient is
 CC afflicted with breast cancer. The breast cancer associated sequences
 CC from the present invention have cytostatic activities and can be used in
 CC gene therapy. The method is useful for diagnosing and treating breast
 CC cancer.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 450 AA;

Query Match 46.6%; Score 1245.5; DB 24; Length 450;
 Best local Similarity 54.1%; Pred. No. 5.5e-108;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPSGTCACTKCEHTRPKPCBLAGFRAFRKGDVVTTILEACENKSKWYRVKHHTSQQEGLAAGAR 106
 Db 8 WPSGTECAKYNFHGTAAEQDQFLPECKGDVLTAVTKDPWYKAKNV-GREGILIPANYQ 66
 QY 107 EREALSADPKLSLMPWFHKSKISGQAVQOLQPPEDEGLYVRESARHPPGRGDIVLCVSFGRDY 166
 Db 67 KREGVKAGTKLSLMPWFHKITRQAERHLYPPETGLEYVRESNPYPGYTICVSCDKV 126
 QY 167 IHYRLHRQHGLTIDEAVFCNLMDMVYKSGKGAICHLVLRKRKGTKSAEELARA 226
 Db 127 EHRYIMHASKLISIDEEVFENLMLVNEHITSDAEGLCIRLKPKMEGVAADEFIRS 186
 QY 227 GWLNLQHHTLGADIGEGFGRGAQVLOQEYQGQKVAKNPKCDVIAQAFLEDETATMKHRE 286
 Db 187 GWALMKKEIQLQQTGKGFRGDMVMLGDYQKGNKVAKVCKTNDAQAFLEASVMTLHS 246
 QY 287 NLVRLLGVILHQ-GLITMEHWSKGNLNFRLRGRAVLNTAQOLQSLHVARGMEIE 344
 Db 247 NLVOLQGIVWEKGIVYTYEMAKGSVLDYLSRSRGSVLLGGDCILKESLSDVCEAMEYIE 306
 QY 345 SKKLVHVDIJAARNILVSEDLVAKVSDFGIKAERKGGLDSSRLPVKWTAPEALKHGKFST 404

XX Sequence 820 AA;

Query Match 36.7%; Score 979.5; DB 22; Length 820;
 Best local Similarity 48.8%; Pred. No. 1.3e-82;
 Matches 191; Conservative 72; Mismatches 123; Indels 5; Gaps 3;

QY 93 TSGEGLLAAGALREREALS-ADPKLSLMPWFHKSKISGQAVQOLQPPEDEGLYVRSAR 151
 Db 407 TAMNHASLSPPTALAPQQGRSRCSRCVKNLAMPWFHGTSITRDEAHLQPREDGFLFVRESTN 466
 QY 152 HPGDYLVCUSFGRDYIHWRLHRQHGLTIDEAVFFCNLMDMVYHYSKDGAICTKLYRPK 211

Db	467	FPGDYTLVCVCFQSKVREHYRVKYLENKLTDDEEFENLGLQVLAHEADAGLCIOLIKCL	526
Oy	212	RKHGTKS---AEBELLARAGWLNLNQHHTLGQAQGEFFGAVLQGQTYLGQKAVAKNIKCD	268
Db	527	PKLGKQBECINSKDFVFDKGWVIFERELQRESIGKGEFSDVMGLGIRNERKAVAKALKDEG	586
Oy	269	TQAQFLBETAVWMKMMQHENLVRLIGWIL-HOGLYIYMEHVSQGNVNLETRGRALVNTA	327
Db	587	AVOKFLABEASWMTLEHDNLVFKFGFLVTFSKHLVTVEYNSKGSLWDYLRSRGROHITKK	646
Oy	328	QLIQFSLHVAGEMYELESKKLVRDAAARNILYSEBDLVARVKSDFGLAKABERKGKJGUSSRLP	387
Db	647	DOLIFAVDTASGKEYLEAKKVKHDLAARNVLSEDCVAKVSDFGLAREECYNYLDVGKLP	706
Oy	388	VKWTPEALKHGFTSKSDWWSGVLLWVFSGRAPHYKMSLKEYSEATEKGYMEPE	447
Db	707	IKWTAPPEALKNGRFNSKNSDMWSFGILLWISFGRVPRYPRIPLADEVKHVEGYMEAPE	766
Oy	448	GPGPVHVLMSQWEAARRPPRPLAELK 478	
Db	767	GCPPEITEMMRQAWDLNPAKPTPEAKVKKL	797

Search completed: July 29, 2003, 09:50:57
Job time : 47 secs

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GenCore version 5.1.6
copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2003, 09:47:52 ; Search time 16 Seconds

(without alignments)
1490.159 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRGSILVSWRAFHGCDSAE..... PASVSGQDADGSTSPRSQEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2671	100.0	507	1 MATK_HUMAN	P42679 homo sapien
2	2332	87.3	505	1 MATK_MOUSE	P41442 mus musculus
3	2221.5	83.2	467	1 MATK_RAT	P41443 ratus norvegicus
4	1253.5	46.9	450	1 CSK_CHICK	P41339 gallus gallus
5	1245.5	46.6	450	1 CSK_RAT	P41340 homo sapiens
6	1242.5	46.5	450	1 CSK_MOUSE	P32577 rattus norvegicus
7	1227.5	46.0	450	1 LCK_CHICK	P41241 mus musculus
8	762.5	28.5	507	1 LCK_MOUSE	P42083 gallus gallus
9	744.5	27.9	508	1 LCK_HUMAN	P06230 mus musculus
10	742.5	27.8	508	1 SRC_RSVR	P06239 homo sapiens
11	735.5	27.5	568	1 SRC_AVISS	P00524 rous sarcoma virus
12	734.5	27.5	557	1 SRC_AVIST	P14084 avian sarcoma and leukosis virus
13	734	27.5	532	1 SRC_CHICK	P00523 gallus gallus
14	733	27.4	526	1 SRC_AVIS	P00525 avian sarcoma virus
15	731.5	27.4	587	1 SRC_AVIS2	P15054 avian sarcoma virus
16	731.5	27.4	523	1 SRC_RSVP	P31993 rous sarcoma virus
17	727.5	27.2	535	1 SRC_HUMAN	P12931 homo sapiens
18	727	27.2	531	1 SRC_XENLA	P13115 xenopus laevis
19	726	27.2	526	1 HCK_HUMAN	P08331 homo sapiens
20	724.5	27.1	526	1 SRC_RSVHL	P25020 rous sarcoma virus
21	724.5	27.1	526	1 SRC_XENLA	P13116 xenopus laevis
22	724	27.1	531	1 ABL_DROME	P00522 drosophila melanogaster
23	724	27.1	526	1 SRC_RSVP	P00526 rous sarcoma virus
24	723.5	27.1	535	1 SRC_RAT	Q9wdq9 rattus norvegicus
25	716.5	26.8	505	1 SRK1_SPOLA	P42086 spongeilla
26	716	26.8	505	1 SRK1_SPOLA	P05480 mus musculus
27	714	26.7	540	1 SRC_MOUSE	P42080 spongilla
28	713	26.7	506	1 SRK4_SPOLA	P42080 spongilla
29	713	26.7	511	1 LYN_RAT	P07014 rattus norvegicus
30	710	26.6	541	1 YES_MOUSE	Q04736 mus musculus
31	710	26.6	543	1 YES_HUMAN	P07347 homo sapiens
32	709	26.5	536	1 FYN_XIPHE	P27446 xiphophorus
33	707	26.5	504	1 HCK_MACFA	Q95m30 macaca fasciata

ALIGNMENTS

RESULT 1	MATK_HUMAN	STANDARD:	PRT:	507 AA.
ID	MATK_HUMAN			
AC	P42679;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)			
DE	(Tyrosine-protein kinase CTK) (Protein kinase HYL) (Hematopoietic			
DE	consensus tyrosine-lacking kinase).			
GN	MATK OR CTK OR HYL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI-TaxID=9606;			
PP				
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=94181267; PubMed=8134117;			
RX	[1]			
RX	SEQUENCE FROM N.A.			
RX	Sakano S., Iwama A., Inazawa J., Ariyama T., Ohno M., Suda T.;			
RX	"Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic consensus tyrosine-lacking kinase).";			
RT	(hematopoietic consensus tyrosine-lacking kinase).";			
RL	Oncogene 11:155-161(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Megakaryocytes;			
RX	MEDLINE=94117408; PubMed=8288563;			
RA	Bennett B.D., Cowley S., Jiang S., London R., Deng B., Grabarek J.,			
RA	Groisman J.E., Goeddel D.V., Avramai H.;			
RA	"Identification and characterization of a novel tyrosine kinase from megakaryocytes.";			
RT	J. Biol. Chem. 269:1068-1074(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95130565; PubMed=7530249;			
RA	Ayraham S., Jiang S., Ota S., Fu Y., Deng B., Dowler L.L.,			
RA	White R.A., Ayraham H.;			
RA	"Structural and functional studies of the intracellular tyrosine kinase MATK gene and its translated product.";			
RT	J. Biol. Chem. 270:1833-1842(1995).			
RL				
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,			
RA	Burkhardt-Schultz K., Gordon L., Diaz J., Ramirez M., Stilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,			
RA	Dandanian L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Attix C., Andreise T., Frankheim M., Antico-Keller G., Coeffield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,			
RA	Ariellano A., Saunders C., Ow D., Nolan M., Truong S., Kobayashi A.,			
RA	Olsen A.S., Carrasco A.V.;			
RA	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.			
RL				
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=EVE;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Strausberg R.L., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,			

RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., DR GO; GO:0008284; P-positive regulation of cell proliferation; TAS.
 RA Hopkins R.F., Jordin H., Moore T., Max S.I., Wang J., Hsieh F., DR GO; GO:0006466; P-protein amino acid phosphorylation; TAS.
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., DR GO; GO:000074; P-regulation of cell cycle; TAS.
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., DR InterPro; IPR000719; prot_kinase.
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., DR InterPro; IPR000980; SH2.
 RA Raha S.S., Louuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., DR InterPro; IPR01422; SH3.
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., DR InterPro; IPR01245; Tyr_P kinase.
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., DR Pfam; PF00065; pkinase_1.
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., DR Pfam; PF00017; SH2_1.
 RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., DR InterPro; IPR000980; SH2.
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., DR PRIMs; PR001; IPR01422; SH3.
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Smallius D.E., DR PRODom; PD00093; SH2_1.
 RA Butterfield Y.S.N., Krzywinski M., Skalska U., Marra M.A., DR SMART; SM00252; SH2.
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length DR PRIMs; PR0019; SH2DOMAIN.
 RA human and mouse cDNA sequences"; RT PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=95022650; PubMed=7936664;
 RA Hamaguchi I., Iwama A., Yamaguchi N., Sakano S., Matsuda Y., Suda T.; RT "Characterization of mouse non-receptor tyrosine kinase gene, HYL.",
 RL Oncogene 9:3371-3374(1994).
 CC -!- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF T-CELL PROLIFERATION.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS MYELOID CELL LINES, DETECTED IN BRAIN AND LUNG.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
 CC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 EMBL: LI8974; RAA15703.1; -;
 DR EMBL; X77278; CAA4493.1; -;
 DR EMBL; S5168; AAC0645.1; -;
 DR EMBL; S75145; AAC0645.1; JOINED.
 DR EMBL; S75147; AAC0645.1; JOINED.
 DR EMBL; S5166; AAC0645.1; JOINED.
 DR EMBL; S75151; AAC0645.1; JOINED.
 DR EMBL; S75153; AAC0645.1; JOINED.
 DR EMBL; S5155; AAC0645.1; JOINED.
 DR EMBL; S7515; AAC0645.1; JOINED.
 DR EMBL; S75158; AAC0645.1; JOINED.
 DR EMBL; S75159; AAC0645.1; JOINED.
 DR EMBL; S75162; AAC0645.1; JOINED.
 DR EMBL; S75164; AAC0645.1; JOINED.
 DR EMBL; AAC00577; AAC06284.1; -;
 DR EMBL; AAC00114; AAC00114.1; -;
 DR PIR; A49865; A49865.
 DR PIR; A55625; A55625.
 DR PDB; 1JHO; 12-SEP-01.
 DR Genew; HNC6; MATK.
 MM; 600038; -.
 GO; GO:0005515; P-protein binding activity; TAS.
 GO; GO:0004713; P-protein tyrosine kinase activity; TAS.
 DR GO; GO:0008283; P-cell proliferation; TAS.
 DR GO; GO:0007198; Pimesoderm development; TAS.

DR GO; GO:0008284; P-positive regulation of cell proliferation; TAS.
 DR GO; GO:0006466; P-protein amino acid phosphorylation; TAS.
 DR GO; GO:000074; P-regulation of cell cycle; TAS.
 DR InterPro; IPR000719; prot_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR01422; SH3.
 DR InterPro; IPR01245; Tyr_P kinase.
 DR Pfam; PF00065; pkinase_1.
 DR Pfam; PF00017; SH2_1.
 DR Pfam; PR0018; SH3_1.
 DR PRIMs; PR001; IPR01422; SH3.
 DR PRIMs; PR0019; SH2DOMAIN.
 DR PRODom; PD00093; SH2_1.
 DR SMART; SM00252; SH2.
 DR SMART; SM00326; SH3.
 DR SMART; SM00219; TYRK_C; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS5002; SH3; 1.
 DR Transferase; Tyrosine-Protein kinase; ATP-binding; SH2 domain; KW SH3 domain; Phosphorylation; 3D-structure.
 FT DOMAIN 58 110
 FT DOMAIN 122 211
 FT DOMAIN 235 482
 FT NP_BIND 241 249
 FT BINDING 262 262
 FT ACT_SITE 352 352
 FT CONFLICT 107 108
 FT CONFLICT 400 400
 FT CONFLICT 466 507
 FT CONFLICT 466 507
 FT PKC_ALTPGGPPAPORTERVEASAWGH (IN REF. 1).
 FT PKC_ALTPGGPPAPORTERVEASAWGH (IN REF. 1).
 SQ SEQUENCE 507 AA; 56469 MW; 85721C6E024575EF CRC64;
 Query Match Best Local Similarity 100.0%; Score 2671; Length 507; Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGRSLSVSWRAFICGDSAEELPRLVSPRSPRLRANHPPPPSARMPIRWRAGPTQCITKCHT 60
 QY 1 MAGRSLSVSWRAFICGDSAEELPRLVSPRSPRLRANHPPPPSARMPIRWRAGPTQCITKCHT 60
 Db 61 RPKPEGLAERRKGDVWILEACENSKWSYRKHHSGQEGILAGAARRERBALSAKDPLS 120
 Db 61 RPKPEGLAERRKGDVWILEACENSKWSYRKHHSGQEGILAGAARRERBALSAKDPLS 120
 QY 121 PWFHKISQEAQVOOLQPPEPDGLFLTVRESARHPGDDYLVCSFGRDWTHYVLHRDGHLTI 180
 QY 121 PWFHKISQEAQVOOLQPPEPDGLFLTVRESARHPGDDYLVCSFGRDWTHYVLHRDGHLTI 180
 Db 181 DEAVFFCNLMVHYSKOKGAICTKLVRPKRGTKSAEEELARRAGMLNQHQHIGAQ 240
 Db 181 DEAVFFCNLMVHYSKOKGAICTKLVRPKRGTKSAEEELARRAGMLNQHQHIGAQ 240
 QY 241 IGEFFGAVLQGETGQYAVKNTKCDVQAQFLEDAVTMKHQHENLYLQLHIGL 300
 Db 241 IGEFFGAVLQGETGQYAVKNTKCDVQAQFLEDAVTMKHQHENLYLQLHIGL 300
 QY 301 YIVMHEVSKGNLNVFLRTRGRALYNTAQOLQFSIHLVAEGMEYLESKKLVHDLARNLIV 360
 Db 301 YIVMHEVSKGNLNVFLRTRGRALYNTAQOLQFSIHLVAEGMEYLESKKLVHDLARNLIV 360
 QY 361 SEDVAKVSDFGLAKKAERGLDSSRLPKWKTAFALKIGKFTSKDSWMSGVILWEPSY 420
 Db 361 SEDVAKVSDFGLAKKAERGLDSSRLPKWKTAFALKIGKFTSKDSWMSGVILWEPSY 420
 QY 421 GRAYPKMSLKEVEAVGYMRPEPGCPGPVHLMSCWEARPPFRKLAELK 480
 QY 421 GRAYPKMSLKEVEAVGYMRPEPGCPGPVHLMSCWEARPPFRKLAELK 480

RESULT 2

MATK_MOUSE	STANDARD;	PRT;	505 AA.
ID	MAIK_MOUSE		
AC	P41242;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Megakaryocyte-associated tyrosine-protein kinase (BC 2.7.1.112) (Tyrosine-protein kinase CTk) (Protein kinase NTK).		
DE	MATK OR CTk OR NTK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1] SEQUENCE OF 41-505 FROM N.A.		
RP	TISSUE=Brain;		
RX	MEDLINE=94195789; PubMed=7511815;		
RA	Klages S., Adam D., Class K., Fargnoli J., Bolen J.B., Penhallow R.C.;		
RA	'Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family';		
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).		
RN	[2] SEQUENCE FROM N.A.		
RP	STRAIN=BALB/C; TISSUE=Thymus;		
RX	MEDLINE=94255451; PubMed=8197166;		
RA	Chow L.M., Jarvis C.D., Hu Q., Nye S.H., Gervais F.G., Veillette A., Matis L.A.;		
RT	"Ntk: a Csk-related protein-tyrosine kinase expressed in brain and T lymphocytes";		
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4975-4979(1994).		
RN	[3] SEQUENCE OF 41-505 FROM N.A.		
RP	STRAIN=DDY/STD;		
RX	MEDLINE=95206787; PubMed=7898936;		
RA	Kaneo Y., Nonoguchi K., Fukuyama H., Takano S., Higashitsuji H., Nishiyama H., Takenawa J., Nakayama H., Fujita J.;		
RT	"presence of alternative 5', untranslated sequences and identification of RT of cells expressing ctk transcripts in the brain and testis";		
RL	Oncogene 10:945-952(1995).		
CC	-I- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION OF HEMATOPOETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF T-CELL PROLIFERATION.		
CC	-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein		
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).		
CC	-I- ALTERNATIVE PRODUCTS:		
CC	Event="Alternative splicing; Named isoforms=2;		
CC	Name=1; IsoId=P41242-1; Sequence=Displayed;		
CC	Name=2; IsoId=P41242-2; Sequence=VSP_004966;		
CC	Note="Minor isoform."		
CC	-I- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, AND TO A LESSER EXTENT IN THE SPLEEN, THE THYMUS AND THE LIVER. ALSO FOUND IN THE T-CELL LINEAGE.		
CC	-I- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK SUBFAMILY.		
CC	-I- SIMILARITY: Contains 1 SH2 domain.		
CC	-I- SIMILARITY: Contains 1 SH3 domain.		

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RESULT 3

ID	MARK_RAT	STANDARD;	PRT;	467 AA.
AC	P41243;			"Identical and characterization of Batk, a predominantly brain-specific non-receptor protein tyrosine kinase related to Csk.";
DT	01-FEB-1995 (Rel. 31, Last sequence update)			J. Neurosci. Res. 38:705-715(1994).
DE	28-FEB-2003 (Rel. 41, Last annotation update)			- FUNCTION: Could play a significant role in the signal transduction of hematopoietic cells. May regulate tyrosine kinase activity of SRC family members in brain.
DE	MEGAKARYOCYTE-ASSOCIATED TYROSINE-PROTEIN KINASE (CTK) (Protein kinase BATK).			- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
GN	MATK OR CTK OR BATK.			- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
OS	Rattus norvegicus (Rat).			- TISSUE SPECIFICITY: Enriched in lymphoid tissues.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX			- SIMILARITY: Belongs to the Tyr family of protein kinases. CSK SRC FAMILY MEMBERS IN BRAIN.
RN	[1]			- SIMILARITY: Contains 1 SH2 domain.
RP	SEQUENCE FROM N.A.			- SIMILARITY: Contains 1 SH3 domain.
RC	STRAINS-SPRAGUE-DAWLEY; TISSUE=Hippocampus;			This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
RX	MEDLINE=95106341; PubMed=7817586;			
RA	Kuo S.S., Moran P., Gripp J., Armanini M., Phillips H.S., Goddard A., Caras I.W.;			
RA	"Identical and characterization of Batk, a predominantly brain-specific non-receptor protein tyrosine kinase related to Csk.";			
RT	J. Neurosci. Res. 38:705-715(1994).			
RL	RA			
CC	- FUNCTION: Could play a significant role in the signal transduction of hematopoietic cells. May regulate tyrosine kinase activity of SRC family members in brain.			
CC	- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC	- SUBCELLULAR LOCATION: Cytoplasmic (Probable).			
CC	- TISSUE SPECIFICITY: Enriched in lymphoid tissues.			
CC	- SIMILARITY: Belongs to the Tyr family of protein kinases. CSK SRC FAMILY MEMBERS IN BRAIN.			
CC	- SIMILARITY: Contains 1 SH2 domain.			
CC	- SIMILARITY: Contains 1 SH3 domain.			

Query Match 83.2%; Score 2221.5; DB 1; Length 467; Best Local Similarity 89.3%; Pred. No. 2e-146; Matches 417; Conservative 27; Mismatches 22; Indels 1; Gaps 1; Query Match 83.2%; Score 2221.5; DB 1; Length 467; Best Local Similarity 89.3%; Pred. No. 2e-146; Matches 417; Conservative 27; Mismatches 22; Indels 1; Gaps 1; DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1. DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1. DR PROSITE: PS50001; SH2; 1. DR PROSITE: PS5002; SH3; 1. DR TRANSFERASE; Tyrosine protein kinase; ATP-binding; SH2 domain; KW SH3 domain; Phosphorylation. FT DOMAIN 22 69 SH3. FT DOMAIN 81 170 SH2. PROTEIN KINASE. FT DOMAIN 194 443 ATP (BY SIMILARITY). NP BIND 200 208 ATP (BY SIMILARITY). FT BINDING 221 221 ATP (BY SIMILARITY). FT ACT-SITE 311 311 BY SIMILARITY. SQ SEQUENCE 467 AA: 51896 MW: 283F5348B5FABF CRC64; DR 61 AAAURQREALSTPKPLSLMPWFGKISQEAQOLQPFPEDGLFLVRESARHCGDYVLCVS 120 DR 162 FGRDVTYHRYVLHRDGHLTIDEAVFFCNLMMDMVHYSKDKGATCTKLYVRPKRGHTKSAAE 221 DR 121 FGDRVHRYVLHRDGHLTIDEAVFCFCNLMDMVHRYTRDGKAICTKLYVRPKRGHTKSAAE 180 DR 222 ELARGWLNLOHLTGQIGEGEGFAGVQLOGEYLQKAVKNKCDVTAQAFIDETAVMT 281 DR 181 ELAKGWLIDLQHQLGAQIGEGEGFAGVQGEYLGQYAVKNKCDVTAQAFIDETAVMT 240 DR 282 KMQHENVYLVLGLVHLHQGYIYVMEHWSKGNLVFLRTGRALVNTAQQLQSLHVAEGME 341 DR 241 KLOHRNLYVRLGLGVHLHQGYIYVMEHWSKGNLVFLRTGRALVNTSQQLQFALHVACME 300 DR 342 YLESKLVLYRDLAARNILVSEDLYKAVSKDFGLAKAE_RKGIDSSRLPVKWTPEALKHGK 400 DR 301 YLESKLVLYRDLAARNILVSEDLYKAVSKDFGLAKAE_RKGIDSSRLPVKWTPEALKHGK 360 DR 401 FTRSDVNSFGVLIWEVESGRAPYKPSLKEYSEAVEGYRMEPPCOPGPVHMLMSC 460 DR 361 FSSKDVSNSFGVLIWEVESGRAPYKPSLKEYSEAVEGYRMEPPDCPGPVHMLGSC 420 DR 461 WEAEPPRPFKRLAKELRELASAGAPASVSDAGSTSRSOEP 507 DR 421 WEAEPPRPFKRLAKELRELASAGAPASVSDAGSTSRSOEP 467 DR

RESULT 4

ID	CSK_CHICK	STANDARD;	PRT;	450 AA.
AC	P412439;			"Identical and characterization of Batk, a predominantly brain-specific non-receptor protein tyrosine kinase related to Csk.";
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC kinase).			
GN	CSK.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Galiius.			
OC	NEOGENTHAE; GALLIFORMES; PHASIANIDA; PHASIANINAE; GALLUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE-BRAIN;			
RX	MEDLINE=92196083; PubMed=1372437;			
RA	Sabe H., Knudsen B., Okada M., Nada S., Nakagawa H., Hanafusa H.;			
RT	"Molecular cloning and expression of chicken C-terminal Src kinase: lack of stable association with c-Src protein";			
PROC	Natl. Acad. Sci. U.S.A. 89:2190-2194(1992).			

PROSITE: PS00109; PROTEIN_KINASE_TYR; 1. DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1. DR PROSITE: PS50001; SH2; 1. DR PROSITE: PS5002; SH3; 1. DR TRANSFERASE; Tyrosine protein kinase; ATP-binding; SH2 domain; KW SH3 domain; Phosphorylation. FT DOMAIN 22 69 SH3. FT DOMAIN 81 170 SH2. PROTEIN KINASE. FT DOMAIN 194 443 ATP (BY SIMILARITY). NP BIND 200 208 ATP (BY SIMILARITY). FT BINDING 221 221 ATP (BY SIMILARITY). FT ACT-SITE 311 311 BY SIMILARITY. SQ SEQUENCE 467 AA: 51896 MW: 283F5348B5FABF CRC64; DR 61 AAAURQREALSTPKPLSLMPWFGKISQEAQOLQPFPEDGLFLVRESARHCGDYVLCVS 120 DR 162 FGRDVTYHRYVLHRDGHLTIDEAVFFCNLMMDMVHYSKDKGATCTKLYVRPKRGHTKSAAE 221 DR 121 FGDRVHRYVLHRDGHLTIDEAVFCFCNLMDMVHRYTRDGKAICTKLYVRPKRGHTKSAAE 180 DR 222 ELARGWLNLOHLTGQIGEGEGFAGVQLOGEYLQKAVKNKCDVTAQAFIDETAVMT 281 DR 181 ELAKGWLIDLQHQLGAQIGEGEGFAGVQGEYLGQYAVKNKCDVTAQAFIDETAVMT 240 DR 282 KMQHENVYLVLGLVHLHQGYIYVMEHWSKGNLVFLRTGRALVNTAQQLQSLHVAEGME 341 DR 241 KLOHRNLYVRLGLGVHLHQGYIYVMEHWSKGNLVFLRTGRALVNTSQQLQFALHVACME 300 DR 342 YLESKLVLYRDLAARNILVSEDLYKAVSKDFGLAKAE_RKGIDSSRLPVKWTPEALKHGK 400 DR 301 YLESKLVLYRDLAARNILVSEDLYKAVSKDFGLAKAE_RKGIDSSRLPVKWTPEALKHGK 360 DR 401 FTRSDVNSFGVLIWEVESGRAPYKPSLKEYSEAVEGYRMEPPCOPGPVHMLMSC 460 DR 361 FSSKDVSNSFGVLIWEVESGRAPYKPSLKEYSEAVEGYRMEPPDCPGPVHMLGSC 420 DR 461 WEAEPPRPFKRLAKELRELASAGAPASVSDAGSTSRSOEP 507 DR 421 WEAEPPRPFKRLAKELRELASAGAPASVSDAGSTSRSOEP 467 DR

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CC
CC
CC
DR
EMBL; X88631; CAA1484; 1; -.

DR PIR; S15094; S15094; -.

DR PDB; 1K9A; 01-MAY-02.

DR InterPro; IPR00719; Prot_kinase.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR01452; SH3.

DR InterPro; IPR01245; Tyr_pk kinase.

DR Pfam; PF00069; kinase; 1.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR PRODOM; PD000001; Prot_kinase; 1.

DR PRODOM; PD000093; SH2; 1.

DR PRODOM; PD000066; SH3; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;

KW SH3 domain; Phosphorylation; 3D-structure.

FT DOMAIN 9 70 SH3.

FT DOMAIN 82 171 SH2.

FT DOMAIN 195 445 PROTEIN KINASE.

FT NP_BIND 201 209 ATP (BY SIMILARITY).

FT BINDING 222 222 ATP (BY SIMILARITY).

FT ACT_SITE 314 314 BY SIMILARITY.

FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

SQ SEQUENCE 450 AA; 50746 MW; 393DC8D737DAG67A CRC64;

Query Match 46.5%; Score 1242.5; DB 1; Length 450;

Best Local Similarity 54.1%; Pred. No. 9.4e-79; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGQICITKCENTRKPKGELAFRAKGKDGVVTLERACENKNSWYRKHHTSOGEGLLAAGALR 106

8 WPGSGTECIARIKYNFHGTAKEDQFLPCKDVLTVAVTKDPNNYKAKNVY-GREGIIPANYQ 66

Db 107 EREAL-SADPKLSTLMWFHGKTSQGARAVQLOPPEGFLYRESAHPGIVLVCYSGFRV 166

67 KREGYKAGTKLKSLSMWFHGKTRGEERLKPPIGGFLYRESTNPQDITLCSCEGKV 126

Qy 167 IHYRVLRDGHLTIBAVFFCNLMDMVHEYSKDKGAICLKVLREPKRKHGTSAEBELARA 226

127 EHRYTMHAKSLISLDEEVYFENMOLVOLYHTTDAGLCTRLIKPKYMEGTVAAQDEFYRS 186

Qy 227 GWLLNLQHILTGAQITGEGERGAVALGLEYLGQKAVRNKTCDDVTAQAFIDETAVMTKMQHE 286

187 GWNALMKKEKLQLQTIGKGERFDVMGLDGYRQNKAQKCIKNDATAQAFLAESVMTLQRHS 246

Qy 287 NLVRLGIVLHQ--GLYVMEHEVHSIGNLWFLRTGRALVNTAQIQLQFSHLVHARGMEYLE 344

Db 247 NLVQLGIVTVEBGGLYIVYEMYARKGSVWYLRSGRSVIGGDCILKFSIDVCEAMEYLE 306

Qy 345 SKKLYHRDLARNLIVSEDLVAKYSDFGLAKAERKGCLDSSRLPVKWTPEALKHGFSTK 404

Db 307 GNNFVYRDLARNLVLESDVNAYAKVSDFGFLTKEASSTDQGKLPVWTPAELAREKFSTK 366

Qy 405 SDVWSRGVILWEVFSYGRAPYPKMSIKEVAEVEKGYRMPPPEPGCPGVAVLMSSCWEAE 464

Db 367 SDWSPGILLMEIISFGRVYPRIPLKDVPPRVERGYKMDAPDGCPPAVVDVMKRNWHL 426

Qy 465 PARRPFKRKLAEKL 478

Db 427 AATRPFFLQLREQL 440

RESULT 7
CSK_MOUSE
ID CSK_MOUSE
STANDARD
PRT; 450 AA.

AC P41-41; Q03143;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)

DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-tyrosine kinase MPR-2).

DE CSK
GN Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10890;
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE="Brain";
RX MEDLINE=9419589; PubMed=7511815;

RA Klaes S., Adam D., Class K., Fargnoli J., Bolen J.B.,

RA Penhallow R.C.;
RA Gilardi-Hebenstreit P., Nieto M.A., Fraim M., Mattei M.-G.,

RA Chestier A., Wilkinson D.G., Charray P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
RT OncoGene 7:2499-2506(1992).

CC - FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.

CC CAN ALSO ACT ON THE LYN AND FYN KINASES.

CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC - SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC - TISSUE SPECIFICITY: UBIQUITOUS, BUT MOST ABUNDANT IN THYMUS AND SPLEEN, AS WELL AS IN NEONATAL BRAIN.

CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK SUBFAMILY.

CC - SIMILARITY: Contains 1 SH2 domain.

CC - SIMILARITY: Contains 1 SH3 domain.

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CC EMBL; U05247; AAA18766; 1; -.

DR EMBL; X57242; CAA40518; 1; -.

DR PIR; 148929;

DR PDB; 1JEG; 31-OCT-01.

DR MGDB; MG1.8857; Csk.

DR InterPro; IPR00719; Prot_kinase.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR InterPro; IPR001245; Tyr_pk kinase.

DR Pfam; PF00069; kinase; 1.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR InterPro; IPR000980; SH2DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR PRODOM; PD000001; Prot_kinase; 1.

DR PRODOM; PD00003; SH2; 1.

DR PRODOM; PD00066; SH3; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

- RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE="leukemic T-cell";
 RX MEDLINE=9608519; PubMed=7495859;
 RA Vogel L.B., Arthur R., Fujita D.J.;
 RT "An aberrant lck mRNA in two human T-cell lines.";
 RL Blochim. Biophys. Acta 1264:168-172(1995).
 RN [6]
- RP SQUENCE FROM N.A.
 TISSUE="Lymph."
 RX MEDLINE=22368257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Grouse L.H., Shemesh C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Atschul S.F., Zeeberg B.R., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Munoz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boutefaud G.G.,
 RA Blakesley R.W., Touchman J.W., Green E., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnerech A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
- RP SEQUENCE OF 13-508 FROM N.A.
 RC TISSUE="Peripheral blood lymphocytes";
 RX MEDLINE=20462621; PubMed=1109097;
 RA Boncristiano M., Majolani M.B., D'Elia M.M., Pacini S., Valensin S.,
 RA Baldari C.T.;
 RT "Defective recruitment and activation of ZAP-70 in common variable
 RT immunodeficiency Patients with T cell defects.";
 RL Eur. J. Immunol. 30:2632-2638(2000).
 RN [8]
- RP SQUENCE OF 367-508 FROM N.A.
 RX MEDLINE=88217332; PubMed=2835736;
 RA Velleca A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
 and other non-lymphoid human tumor cell lines.";
 RL Oncogene Res. 1:357-374(1987).
 RN [9]
- RP SQUENCE OF 374-508 FROM N.A.
 RX MEDLINE=8700726; PubMed=3489486;
 RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
 RA Linna T.-J.;
 RT "Human T-lymphocytes express a protein-tyrosine kinase homologous to
 RT p56LSTR.";
 RL Blochim. Biophys. Acta 888:286-295(1986).
 RN [10]
- RP SQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89056891; PubMed=8505479;
 RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;
 RT "Structure of the murine lck gene and its rearrangement in a murine
 RT lymphoma cell line.";
 RL Mol. Cell. Biol. 8:3058-3064(1988).
 RN [11]
- RP SQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89313764; PubMed=27887474;
 RA Takadera T., Leung S., Germino A., Koga Y., Takihara Y.,
 RA Miyamoto N.G., Mak T.W.;
 RT "Structure of the two promoters of the human lck gene: differential
 accumulation of two classes of lck transcripts in T cells.";
 RL Mol. Cell. Biol. 9:2173-2180(1989).
 RN [12]
- RP MASS SPECTROMETRY.
 RC TISSUE="Breast cancer";
- RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zweebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 protein expression map database.";
 RL Proteomics 2:2112-223(2002).
 RN [13]
- RP INTERACTION WITH PI3K.
 RX MEDLINE=94067101; PubMed=7504174;
 RA Vogel L.B., Fujita D.J.;
 RT "The SH3 domain of p56lck is involved in binding to
 phosphatidylinositol 3'-kinase from T lymphocytes.";
 RL Mol. Cell. Biol. 13:7408-7417(1993).
 RN [14]
- RP INTERACTION WITH KHDRBS1.
 RX MEDLINE=95155308; PubMed=7852312;
 RA Vogel L.B., Fujita D.J.;
 RT "p0 phosphorylation and binding to p56lck is an early event in
 interleukin-2-induced onset of cell cycle progression in
 T-lymphocytes.";
 RL J. Biol. Chem. 270:2506-2511(1995).
 RN [15]
- RP PHOSPHORYLATION OF TYR-504.
 RX MEDLINE=9237326; PubMed=1639064;
 RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
 RA Arelein K.E., Autero M., Burn P., Alitalo K.;
 RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
 RT down regulates its catalytic activity.";
 RL EMBO J. 11:2919-2924(1992).
 RN [16]
- RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
 RX MEDLINE=94203291; PubMed=7512222;
 RA Eck M.J., Attewell S.K., Shoelson S.E., Harrison S.C.;
 RT "Structure of the regulatory domains of the Src-family tyrosine
 kinase lck.";
 RL Nature 368:764-769(1994).
 RN [17]
- RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
 RX MEDLINE=95173978; PubMed=7532720;
 RA Mikol V., Baumann G., Keller T.H., Manning U.M., Zurini M.G.M.;
 RT "The crystal structures of the SH2 domain of p56lck complexed with
 RT two phosphopeptides suggest a gated peptide binding site.";
 RL J. Mol. Biol. 246:344-355(1995).
 RN [18]
- RP X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225.
 RX MEDLINE=96177765; PubMed=8804142;
 RA Tong L., Warren T.C., King J., Betageri R., Rose J., Jakes S.;
 RT "Crystal structures of the human p56lck SH2 domain in complex with
 RT two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution.";
 RL J. Mol. Biol. 261:601-610(1996).
 RN [19]
- RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 118-225.
 RX MEDLINE=9832059; PubMed=9885372;
 RA Tong L., Warren T.C., Lukas S., Schembri-King J., Betageri R.,
 RA Proudfoot J.R., Jakes S.;
 RT "Carboxymethyl-phenylalanine as a replacement for phosphotyrosine in
 RT SH2 domain binding.";
 RL J. Biol. Chem. 273:20238-20242(1998).
 RN [20]
- RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500.
 RX MEDLINE=9710052; PubMed=8845479;
 RA Yamaguchi H., Hendrickson W.A.;
 RT "Structural basis for activation of human lymphocyte kinase Lck upon
 RT tyrosine phosphorylation.";
 RL Nature 384:484-489(1996).
 CC -1 FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -1 tyrosine phosphorylation.
 CC -1 SUBUNIT: Binds to phosphatidylinositol 3'-kinase (PI3K) from T
 CC -1 lymphocytes through its SH3 domain and to the tyrosine
 CC -1 phosphorylated form of KHDRBS1/p70 through its SH2 domain.
 CC -1 SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER

KW	Tyrosine-protein kinase; Oncogene; transferase; Phosphorylation;	CC	tyrosine phosphate.
FT	ATP binding; Myristate; SH3 domain; SH2 domain.	CC	- I - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
FT	LIPID	CC	SUBFAMILY.
FT	DOMAIN	CC	- I - SIMILARITY: Contains 1 SH2 domain.
FT	148	SH3.	- I - SIMILARITY: Contains 1 SH3 domain.
FT	245	SH2.	- I - SIMILARITY: Contains 1 SH3 domain.
FT	267	PROTEIN KINASE.	- I - SIMILARITY: Contains 1 SH3 domain.
FT	NP-BIND	DR	PIR; B25375; TVRS2.
FT	273	ATP (BY SIMILARITY).	DR
FT	BINDING	DR	HSSP; P00533; 2PK.
FT	295	ATP (BY SIMILARITY).	DR
FT	ACT-SITE	DR	InterPro; IPR00719; Prot_kinase.
FT	386	BY SIMILARITY.	DR
FT	MOD-RES	DR	InterPro; IPR00880; SH2.
FT	416	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).	DR
SEQUENCE	568 AA; 63632 MW; 1377DB12IF7098 CRC64;	DR	InterPro; IPR01245; Tyr_Pkinase.
Query Match	27.5%; Score 734.5; DB 1; Length 568;	DR	InterPro; IPR01452; SH3.
Best Local Similarity	39.5%; Pred. No. 1.7e-43; Matches 168; Conservative 75; Mismatches 155; Indels 27; Gaps 10;	DR	InterPro; IPR0162; SH2.
Db	99 DLSFKKGGERLQTYNNTBG-DWMLAHLSTGTGQYVIPSINYVAPSDTOAE-----ENYFG 151	DR	PFam; PF00017; SH2; 1.
Qy	66 ELAFRKGVWTLACENKSMWYRKHITSQGQGLANGALRREALSADPKLSLMPWFHG 125	DR	PFam; PF00018; SH3; 1.
Db	126 KISGQEAQVQLQQPED--GLFLYRESARHPGDVLCVS---FGRDVHYRLHRD-GH 177	DR	PRINTS; PR00452; SH3DOMAIN.
Qy	152 KITRRESEPLLNPENRGTFLVRESNTKGAYCLSVSDFDNRAGLAVKHYKIRKLDSGG 211	DR	PRINTS; PR00452; SH3; 1.
Db	178 LTIDEAVEFFCNLMDVMEYNSKRGATCTKL--VRPKRKHTGSAEELARAGWLNLQHL 235	DR	PRODOM; PD000093; SH2; 1.
Db	212 FITSRTOFSSLQQLVAVYISKHADGLCHRLTNVCPTSKPQTG---LAKDWEIPRESL 267	DR	PRODOM; PD000066; SH3; 1.
Qy	236 TUGAQIGERGEGFAGAVLOGYLG-OKVAVKNIK-CDVTAQAFLEDETAVMTKMOHENLVLIG 293	DR	SMART; SM00252; SH2; 1.
Db	268 RLEVKGOGCGFGEWMGTTWNGT'RAIKTLKPGTMSPAFQLAQVKKLRHEKLVYLA 327	DR	PROSITE; PS00017; PROTEIN_KINASE_ATP; 1.
Qy	294 VILHQGLIVMEAVSKGNLNVNLTGRNALVTAQLQFSLHVAGEMEYLESKKLYRDL 353	DR	PROSITE; PS00019; PROTEIN_KINASE_TYR; 1.
Db	328 VVSEEPITVIVTEYMSKSLDPLKGEMGKYLRLPOLVDMAQIASGHMAYVERMVYVHDL 387	DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
Qy	354 AARNILVSEDLVAKVSDGLAKA---ERKGIDSSRLPKWTAPEALKHGFTSKDWS 409	DR	PROSITE; PS00001; SH2; 1.
Db	388 RAANILVGENLICKVAKPGLARLIEDNEYTAROGAKPKIWKTAPEALKHGFTSKDWS 447	DR	PROSITE; PS00002; SH3; 1.
Qy	410 FGVLWEVFSYGRAPYKMSLKEVEAKGKTRMEPEPGCPGPVHIMSSWEAEARRP 469	DR	PROSITE; PS00017; PROTEIN_KINASE_ATP; 1.
Db	448 FGILLTEITTKGRVVPICGMVNREVLQDVERGIRMPCCPECPCPESLHDLMCQCWRKDPEERP 507	DR	PROSITE; PS00017; PROTEIN_KINASE_TYR; 1.
Qy	470 PERKL 474	DR	PROSITE; PS00019; PROTEIN_KINASE_ATP; 1.
Db	508 TFEVL 512	DR	PROSITE; PS00017; PROTEIN_KINASE_TYR; 1.
RESULT 13		DR	PROSITE; PS00017; PROTEIN_KINASE_ATP; 1.
SRC_AVIST		DR	PROSITE; PS00017; PROTEIN_KINASE_TYR; 1.
ID	SRC_AVIST	STANDARD;	PRT; 557 AA.
AC	P14085;		
DT	01-JAN-1990 (Rel. 13' Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Tyrosine-protein kinase transforming protein SRC (EC 2.7.1.112) (P60-		
DE	SRC).		
GN	OS		
OS	Avian sarcoma virus (strain S2), Retrovirus; Retroviridae; Avian type C retroviruses.		
OC	Viruses; Retrovirus; Retroviridae; Avian type C retroviruses.		
OX	NCBI TaxID=11882;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=87064539; PubMed=3097513;		
RA	Ikawa S., Hagiwara-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K., Mol. Cell. Biol. 6:2420-2428 (1986).		
RT	-!- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES IN VITRO.		
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein		

Db	508 TFEYLQAFLEDYLGILAWTPWEDKQEGPRGETASNKQE	RA	Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
RT	"Tyr527 is phosphorylated in pp60c-src: implications for regulation.";	RT	
RL	Science 231:1431-1434(1986).	RL	
RP	X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.	RP	
ID	SRC_CHICK STANDARD; PRT; 532 AA.	ID	SRC_CHICK STANDARD; PRT; 532 AA.
AC	P0053; Q90992; Q91343; Q91345; Q92013; Q98915;	AC	P0053; Q90992; Q91343; Q91345; Q92013; Q98915;
DT	21-JUL-1986 (Rel. 01, Created)	DT	21-JUL-1986 (Rel. 01, Created)
DT	15-JUL-1999 (Rel. 38, Last sequence update)	DT	15-JUL-1999 (Rel. 38, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)	DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src) (c-Src).	DE	Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src) (c-Src).
GN	GN	GN	GN
OS	Gallus gallus (Chicken).	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
OC	OC	OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
OX	NCBL_TAXID=9031;	OX	NCBL_TAXID=9031;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=8315564; PubMed=6299580;	RX	MEDLINE=93279385; PubMed=8504863;
RA	Takeya T., Hanafusa H.;	RA	Yu H., Rosen M.K., Schreiber S.L.;
RT	"Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";	RT	"1H and 15N assignments and secondary structure of the Src SH3 domain.";
RT	Cell 32:881-890(1983).	RT	J. Mol. Biol. 274:75-77(1997).
RL	[2]	RL	[10]
RP	REVISION TO 525.	RP	STRUCTURE BY NMR OF 80-139.
RA	Takeya T., Hanafusa H.;	RA	MEDLINE=95063992; PubMed=7526465;
RL	Cell 34:319-319(1983).	RA	Feng S., Chen J.K., Yu H., Simon J.A., Schreiber S.L.;
CC	[3]	RT	"Two binding orientations for peptides to the Src SH3 domain: development of a general model for SH3-ligand interactions";
CC	SEQUENCE FROM N.A., AND PHOSPHORYLATION OF TYR-415 AND TYR-435.	RL	Science 265:1241-1247(1994).
RX	MEDLINE=97008971; PubMed=8856081;	CC	-I- FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED TO HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS AND MACROPHAGES.
RA	Weijland A., Neubauer G., Courtneyde S.A., Mann M., Wierenga R.K., Superti-Furga G.;	CC	-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
RT	The purification and characterization of the catalytic domain of src expressed in <i>Schizosaccharomyces pombe</i> . Comparison of c-src unphosphorylated and tyrosine phosphorylated species.;	CC	tyrosine phosphate.
RT	Eur. J. Biochem. 240:756-764(1996).	CC	-I- ENZYME REGULATION: BECOMES ACTIVATED WHEN ITS MAJOR TYROSINE PHOSPHORYLATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE C-TERMINAL END OR BY OTHER MUTATIONS.
RN	[4]	CC	-I- PIM: Phosphorylated on TYR-526 by c-src kinase (CSKI). The phosphorylated tail interacts with the SH2 domain thereby repressing kinase activity (By similarity).
RP	SEQUENCE OF 1-18 AND 484-533 FROM N.A.	CC	-I- MISCELLANEOUS: POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.
RX	MEDLINE=91304019; PubMed=1712905;	CC	-I- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.
RA	Doria T., Levy J.B., Kang L., Brugge J.S., Wang L.H.;	CC	-I- SIMILARITY: Contains 1 SH2 domain.
RT	"Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and possible mechanism for the genesis of the 3' end of v-src."	CC	-I- SIMILARITY: Contains 1 SH3 domain.
RT	Mol. Cell. Biol. 11:4165-4176(1991).	CC	-----
RN	[5]	CC	-----
RP	ATP-BINDING SITE.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RX	MEDLINE=8427051; PubMed=6431300;	CC	-----
RA	Kamps M.P., Taylor S.S., Sefton B.M.;	CC	-----
RT	"Direct evidence that oncogenic tyrosine kinases and cyclic AMP-dependent protein kinase have homologous ATP-binding sites.";	CC	-----
RT	Nature 310:589-592(1984).	CC	-----
RN	[6]	DR	EMBL: V00402; CAA23696.1; -
RP	PHOSPHORYLATION.	DR	EMBL: J00844; AAB19353.2; -
RX	MEDLINE=86028181; PubMed=2996780;	DR	EMBL: A00630; TVCHS.
RA	Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D., Hunter T., Protein kinase C phosphorylates pp60src at a novel site.;	DR	EMBL: S43604; AAD13831.1; -
RA	Erikson R.L., Bishop J.M., "Characterization of sites for tyrosine phosphorylation in the transforming protein of Rous sarcoma virus (pp60c-src) and its normal cellular homologue (pp60c-src)." Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).	DR	EMBL: S43616; AAD13835.1; -
RT	Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).	DR	EMBL: S43587; AAD13830.1; -
RN	[8]	DR	EMBL: S43609; AAD13832.1; -
RX	PHOSPHORYLATION OF TYR-526.	DR	EMBL: S43614; AAD13834.1; -
RX	MEDLINE=86151652; PubMed=2420005;	DR	EMBL: S43579; AAB19353.2; -
RP	PDB; 1F2F; 06-JUL-00.	DR	PDB; 1F2F; 06-JUL-00.

QY	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR000980; SH2.
DR	InterPro; IPR001452; SH3.
DR	InterPro; IPR001245; Tyr_pk kinase.
DR	Pram; PR00059; Pkinase; 1.
DR	Pram; PR00017; SH2; 1.
DR	PR0018; SH3; 1.
DR	PRINTS; PRO0401; SH2DOMAIN.
DR	PRINTS; PRO0452; SH3DOMAIN.
DR	PRINTS; PR00109; TYRKINASE.
DR	Prodrom; PD000001; Prot_kinase; 1.
DR	Prodrom; PD000003; SH2; 1.
DR	Prodrom; PD000066; SH3; 1.
DR	SMART; SM00252; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00219; TYRK; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS50002; SH3; 1.
KW	Tyrosine-protein kinase; Proto-oncogene; Phosphorylation; Transf erase; ATP-binding; Myristate; SH3 domain; SH2 domain; 3D-structure.
FT	INIT_MET 0
FT	LIPID 1 0
FT	DOMAIN 80 141
FT	DOMAIN 147 244
FT	DOMAIN 266 519
FT	MOD_RES 11 11
FT	NP_BIND 272 280
FT	BINDING 294 294
FT	ACT_SITE 385 385
FT	MOD_RES 415 415
FT	MOD_RES 435 435
FT	MOD_RES 526 526
FT	CONFLICT 300 300
FT	CONFLICT 500 500
FT	STRAND 84 87
FT	STRAND 91 91
FT	STRAND 98 98
FT	TURN 101 101
FT	TURN 103 104
FT	STRAND 106 108
FT	STRAND 117 122
FT	TURN 123 125
FT	STRAND 128 132
FT	HELIX 133 135
FT	STRAND 136 138
FT	TURN 139 140
FT	HELIX 142 144
FT	TURN 146 147
FT	STRAND 148 150
FT	HELIX 154 151
FT	TURN 162 162
FT	TURN 168 169
FT	STRAND 171 175
FT	TURN 180 181
FT	STRAND 183 188
FT	STRAND 191 191
Query Match	27.4%; Score: 733; DB: 1; Length: 532;
Best Local Similarity	37.9%; Pred. No. 2e-43; Gaps: 11;
Matches	173; Conservative: 78; Mismatches: 42; Indels: 163; Gaps: 11;
QY	66 ELAFRKGDVWTLBACENKSWRVRKHHSQEGLLAAGLREREALSADPKLSQLMPWTH 125
Db	98 DLSPKKGERLQLQPPEP-GFLFLYRESARHPGDVKLCVS---FGDVIHYRLHRD-GH 177
QY	126 KISQGEAVQOLQPPEP-GFLFLYRESARHPGDVKLCVS---FGDVIHYRLHRD-GH 177
151 KIRRESERLLNPENPRTGFLYRESETKGAYCLSVSDFDNAKGKLVHKYKIRKLDSGG 210	
QY	178 LTIDEAVFCNLNDMVEHYSKRGAICTKL-VPRPKRGHTKSAEELARAGWLNLQHL 235
Db	211 FYTTSRTOFSSILQLVAVYSKHADGLCHRLTNCPTSKPQTG---LAKDAWEIPRESL 266
Db	236 TLGAQIGCEGEFFGAVLQGBYLG-QKVAKNIK-CDVTAQAFLEDTAVTMQHBNLYRLG 293
QY	354 AARNITLYSEDDVAKVSDGFLAKA---ERKGDDSRPLVKWMAPEALKHGKHTSKSDWS 409
Db	387 RAANILNGENLYVCKVADGLKARLIEDNEYTARQAKEPKIKWAAPEALYGRETIKVWS 446
QY	410 FGVLWEEFSYGRAPYPRMSLEVEAKVGKRMPEPGCPCPVPHUMSSCQEAEPARR 469
Db	447 FGILITELTTKGRPYPMQVNRYDVERGRTPCPCPSLHDIMCQWRKDDEPR 506
QY	470 PFKLAKEIARELRSAGAPASVSGDAGSTSPRSQ 505
Db	507 TFEVLOAFL---EDFTSTPQY 527.
RESULT	15
ID	SRC_AVISR
STANDARD	
PRT	526 AA.
AC	PR0025;
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Tyrosine-protein kinase transforming protein SRC (EC 2.7.1.12) (P60-
GN	V-SRC.
OS	Avian sarcoma virus (strain rASV141).
OC	Viruses; Retroviruses; Retroviridae; Avian type C retroviruses.
OX	NCBI_TaxID=11894;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=83059858; PubMed=6292477;
RA	Takeya T., Feldman R.A., Hanafusa H.;
RT	"DNA sequence of the viral and cellular src gene of chickens: 1. Complete nucleotide sequence of an EcorI fragment of recovered avian sarcoma virus which codes for gp37 and p60src.";
RT	J. Virol. 44:1-11(1982).
RN	[2]
RP	PHOSPHORYLATION OF TYR-416.
RX	MEDLINE=811220979; PubMed=62643320;
RA	Neill J.C., Ghysdael J.J., Vogt P.K., Smart J.E.;
RT	"Homologous tyrosine phosphorylation sites in transformation-specific gene products of distinct avian sarcoma viruses.";
RL	Nature 291:675-677(1981).
CC	-1- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES IN VITRO. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBAMILY.
CC	-- SIMILARITY: Contains 1 SH2 domain.
CC	-- SIMILARITY: Contains 1 SH3 domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL; K00928; AA42505.1; -

DR PDB; 1QWE; 08-MAR-96.

Job time : 19 secs

DR	InterPro; IPR001796; Prot_kinase.
DR	InterPro; IPR001980; SH2.
DR	InterPro; IPR011452; SH3.
DR	InterPro; IPR01245; Tyr_pk kinase.
DR	Pfam; PF00069; Pkinase; 1.
DR	Pfam; PF00017; SH2; 1.
DR	PRINTS; PR00401; SH2DOMAIN.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PRINTS; PR0109; TYRKINSE.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	ProDom; PD000093; SH2; 1.
DR	ProDom; PD00066; SH3; 1.
DR	SMART; SM00252; SH2; 1.
KW	SMART; SM00320; SH3; 1.
FT	SMART; SM00219; TYRK; 1.
FT	LIPID; 2; PROTEIN_KINASE_ATP; 1.
FT	DOMAIN; 81; MYRISTATE.
FT	DOMAIN; 148; SH3.
FT	DOMAIN; 267; PROTEIN_KINASE.
FT	NP_BIND; 273; ATP (BY SIMILARITY).
FT	BINDING; 295; ATP (BY SIMILARITY).
FT	ACT_SITE; 386; BY SIMILARITY.
MOD_RES	416; PHOSPHORYLATION (ATTO-SEQUENCE
SQ	526 AA; 58878 MW; PDB3905F80233E49 CRC64;
Query	Match
Best Local Similarity	27.4%
Matches	39/28; Pred. No. 2.5e-43;
Matches	168; Conservative
QY	66 BLAFRKGDVVTILECENKSWRYKHTSQEGGLIAAGALREREREALASADPKLSIAMPWFHG 1255
Db	99 DLSFRKKERHQIQVNNTEG-DWMLAHLSTTGTQGVIPSPNVAPSNSIQAE-----EWFG 1515
QY	126 KISGBQAVQOLQPRED--GLFLVRSSARHPIGDYIVCS----FGRDWHYVHLRD-GH 177
Db	152 KTRRESERELLNPNPMPRGFLVRSSETKGAYCLSVSDDENAKGHLNHYKTKRLDGG 211
QY	178 LTIDEKVFNCNLMDMVEHYSKDGAICTLU--VPRKRKGHTSAEEELARAGWLNQLH 2355
Db	212 FYITSRSTQFSSLQQLVAVYSSKHADGLCHRLTNVCPSTSXPOTOG---LAKDAWEIPRESL 267
QY	236 TLGAQIGEGFGEVAVIQLGEYIG-QKVAVKNIK-CDVTAQAFDELTAWTMTHQHENLVRLLG 293
Db	268 RLEVLKGQGCGFGEVWNGTWTRVAKIUKPGTMSPRFQEAQYMKURHERKLYQLYA 327
QY	294 VILHQLGYTMEHVSKGNLVNFLTRGRALVNTAOLFLSLHVGEMLYESLESKLHRL 353
Db	328 VWSERFIIYTYTEYMSKGSLSLDFLKGEMKYLRLPQVDMQAJASGMAYVERMYVHROL 387
QY	354 AARNITIVSDELVAKVSKSDFGLAKA---ERRKLDSRSLPVKWTDEALKHGKFTSKDW 405
Db	388 RAANTILGENLNUCKVADFLGARLARLIEDNEYTAROGAKFKPITKWTAAPEALYGRETTSKDW 447
QY	410 FGVLIWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPGEGGPVPHVLMSCWEAEPARRP 465
Db	448 FGILILLETJTSKGRVYFGMNGEVLDRVERGYRMPCCPCPESLHDLMQCWRDRPEEP 507
OY	470 PFRKLAKL 478
Db	508 TFEYLAQQL 516

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:48:37 ; Search time 44 Seconds

(without alignments)
2973.470 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRGSILVSWRAFHGCDSAE.....PASVGQDADGSTSPRSQEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23;*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriip:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query	Match Length	DB ID	Description	RESULT 1	ALIGNMENTS
1	2544	95.2	523	4	Q9NST8	Q9NST8 PRELIMINARY; PRR; 523 AA.		
2	2385.5	89.3	465	4	Q6176	Q9NST8; DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)		
3	2277.5	85.3	511	4	Q61103	DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)		
4	2214.5	82.9	465	11	Q966H7	DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)		
5	2214.5	82.9	465	11	P70223	DE HYPOTHEICAL PROTEIN (Fragment). GN DKFZP43N1212.		
6	1243.5	46.6	450	13	Q8VCL1	OS Homo sapiens (Human).		
7	1216.5	45.5	450	13	Q73786	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
8	1004.5	37.6	485	5	Q9J1Z0	OC NCBITaxonID=9606;		
9	979.5	36.7	723	5	Q9VRK8	RN [1]		
10	976.5	36.6	467	5	Q77132	RP SEQUENCE FROM N.A.		
11	753.5	28.1	509	11	Q91X65	RC TISSUE=Testis;		
12	742.5	27.8	526	13	Q93080	RA Duesterhoeft A., Lauber J., Mewes H.-W., Weil B., Wiemann S.; DR Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.		
13	742	27.8	502	13	Q8QGJ9	CC -I - SIMILARITY: CONTAINS 1 SH3 DOMAIN.		
14	737.5	27.6	509	6	Q95m32	DR EMBL: ALJ37754; CAB709061; -.		
15	736	27.6	545	6	Q8B362	DR HSSP; P11362; 1FGK.		
16	735.5	27.5	509	6	Q95KR7	DR InterPro; IPR000719; Prot_kinase.		
						DR InterPro; IPR000980; SH2.		
						DR InterPro; IPR001452; SH3.		
						DR InterPro; IPR001245; Tyr_pk kinase.		
						DR Pfam; PF00069; Pkinase; 1.		
						DR Pfam; PF00017; SH2; 1.		
						DR Pfam; PF00018; SH3; 1.		
						DR PRINTS; PR00041; SH2DOMAIN.		
						DR PRINTS; PR00109; TYRKINSE.		
						DR PRODom; PR00001; PROT_kinase; 1.		
						DR PRODom; PD000093; SH2; 1.		
						DR SMART; SM00252; SH2; 1.		
						DR SMART; SM00326; SH3; 1.		
						DR SMART; SM00219; TYRK; 1.		
						DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
						DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
						DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		

DR PROSITE; P50002; SH3; 1.
 KW Hypothetical protein; ATP-binding; Kinase; SH3 domain; Transferase;
 Tyrosine-protein kinase.
 FT NON_TER 1
 SEQUENCE 523 AA; 5776 MW; C246280FD7890AFE CRC64;

Query Match 95.2%; Score 2544; DB 4; Length 523;
 Best Local Similarity 96.4%; Pred. No. 3.7e-198; Indels 12; Gaps 1;
 Matches 488; Conservative 1; Mismatches 5; Indels 12; Gaps 1;

Qy 2 AGRCSLVSWRAFPGCDSAEELPRVSPRLRANKHPPPSARMPIRRWAPGTOITKCBTR 61
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 30 AGRG-----SGAPPBGSVSPRFLRWHPPPSARMPIRRWAPGTOITKCBTR 77
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 62 PKGELAFRKGDVVTILEACENSKWYRKHHHTSGQEGILAGALRERBALSAKPUSLMP 121
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 78 PKGELAFRKGDVVTILEACENSKWYRKHHHTSGQEGILAGALRERBALSAKPUSLMP 137
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 122 WFGKISQEAQAVQLOPPEPDGLFLVRSSAHRPGDYVLCVSFSERDVHYVRLRDGHLTID 181
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 138 WFGKISQEAQAVQLOPPEPDGLFLVRSSAHRPGDYVLCVSFSERDVHYVRLRDGHLTID 197
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 182 EAFFCNLMDMVEHYSKDKGAICTKLYRKHKGTKSAAEELARAGHNLQLHTLGQI 241
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 198 EAFFFCNLMVHDMVEHYSKDKGAICTKLYRKHKGTKSAAEELARAGHNLQLHTLGQI 257
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 242 GEGEFFGAVLQGEVLGQKAVVKNIKCDTAQAFLEDETAVMTKMOHENLVRLLGVLHGGY 301
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 258 GESEFFGAVLQGEVLGQKAVVKNIKCDTAQAFLEDETAVMTKMOHENLVRLGVHLGGY 317
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 302 IVMEVHVGNLVFLRTRGRALVNTAQQLQFSHVACEMEYSEKKLVHDLAARNLVS 361
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 318 IVMEVHVGNLVFLRTRGRALVNTAQQLQFSHVACEMEYSEKKLVHDLAARNLVS 377
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 362 EDLVAKYSDPGLAKAERKGQLDSSRLPKWYKTAPEALKHKGKFTSKDVSWSFGVLUWEVSYG 421
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 378 EDVAKYSDPGLAKAERKGQLDSSRLPKWYKTAPEALKHKGKFTSKDVSWSFGVLUWEVSYG 437
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 422 RADYPKMSIKEVSEAVEKGYRMEPPCGPGVPHLMSQWEAEPARPPFRKLAELARE 481
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 438 RADYPKMSIKEVSEAVEKGYRMEPPCGPGVPHLMSQWEAEPARPPFRKLAELARE 497
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 482 LRGARAPSWSGQDAGSTSRSQEP 507
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 498 LRSAGARAPSWSGQDAGSTSRSQEP 523
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 RESULT 2
 Q16176 PRELIMINARY; PRT; 465 AA.
 AC 016176; Lal, D.B.K., Lloyd A., Kawamura M., Chen Y.Q., Zhang X.,
 OC 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Lsk protein.
 GN LSK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=94268844; PubMed=7516063;
 RA McIcar, D.W., Lal, B.K., Lloyd A., Kawamura M., Chen Y.Q., Zhang X.,
 RA Staples, J.E., Ortaldo, J.R., O'Shea, J.J.;
 RT "Molecular cloning of lsk, a carboxyl-terminal src kinase (csk) related gene, expressed in leukocytes.", Oncogene 9:2037-2044(1994).
 RL -|- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC DR S71669; AAB3095.1; -
 DR HSSP; P11362; IFRS.
 DR InterPro; IPR000719; prot_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR000980; SH2.

DR InterPro; IPR01452; SH3.
 DR InterPro; IPR01245; Tyr_Pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF0018; SH3; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKc; 1.
 DR PROSITE; P50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; P50001; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; P50002; SH2; 1.
 DR ATTP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 465 AA; 51908 MW; 504B4E8078320C35 CRC64;

Query Match 89.3%; Score 2385.5; DB 4; Length 465;
 Best Local Similarity 98.1%; Pred. No. 2.4e-185; Indels 6; Gaps 1; Matches 457; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 42 MPTRRWAPGTOITKCBTRPKGELAFRKGVVTILEACENSKWYRKHHHTSGQEGILLA 101
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 61 AGALREREALSADPKSLMPWPHGKTSQEAQVQLOPPEPDGLFLVRSEGGHPGDYVLCVT 120
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 162 FGDRVHYVRLHDGLHTIDEAVFFCNLMVHDMVEHYSKDKGAICTKLYRKHKGTSAE 221
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 121 FGDRVHYVRLHDGLHTIDEAVFFCNLMVHDMVEHYSKDKGAICTKLYRKHKGTSAE 281
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 222 ELARGWILNLOHLTIGAQIGIGESEFFGAVLQGEVLYGQKAVVKNIKCDTAQAFLETAVMT 281
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 181 ELARGWILNLOHLTIGAQIGIGESEFFGAVLQGEVLYGQKAVVKNIKCDTAQAFLETAVMT 239
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 282 KMOKENLVRLGLSVLHOGCLYTYMEHVRGKNLYNFLTRGRALVNTAQQLQFSHLVREGME 341
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 240 KMOKENLVRLGLSVLHOGCLYTYMEHVRGKNLYNFLTRGRALVNTAQQLQFSHLVREGME 299
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 342 YLSKLVHDLAARNLTVLSEDVAKYSDFEGLAKAERKGQLDSSRLPKWTAPEALHGKF 401
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 300 YLSKLVHDLAARNLTVLSEDVAKYSDFEGLAKAERKGQLDSSRLPKWTAPEALHGKF 359
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 402 TSKSDWSFGVLUWEVSYGAVPYSKLSKESEAVKGYRMEPPCGPGVPHLMSCW 461
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 360 TSKSDWSFGVLUWEVSYGAVPYSKLSKESEAVKGYRMEPPCGPGVPHLMSCW 419
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Qy 462 EAEPARRDPFRKLAELRSAGAPASVSGQDAGSTSRSQEP 507
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 420 EAEPARRDPFRKLAELRSAGAPASVSGQDAGSTSRSQEP 465
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 RESULT 3
 Q04103 PRELIMINARY; PRT; 511 AA.
 ID 064103; PRELIMINARY; PRT; 511 AA.
 AC 064103;
 OC 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE VNK protein.
 GN VNK.
 OS Mus_sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10055;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=9517894; PubMed=7874011;
 RA Eishler, M.A., Krivtsov, A.V., Beliavskii, A.V., Visser, J.V.,
 RA "VNK-a new gene for nonreceptor protein-tyrosine kinase, expressed

QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281	QY	42 MPTRRWAPGTOCTTKCEHTTRPKPGELAFRAKGVDWTLFACENSWYRKHTSGQEGLLA	101
Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239	Db	1 MPT-RWAPGTOCTMCVKCNSRSPKGELAFRAKGVDWTLFACEDKSWYRAKHGSQEGLLA	59
QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341	QY	102 AGALREREALSAPPKLSLMPWFEGKISQEAQVOLPPEGLTLYRESARHKGDYVLCVS	161
Db	240 KLOHRNLVLRLGVILHGLYIVMHEVKSGNLNVNLFTRGRALYSTSQLQFALHVACME	299	Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
QY	342 YLESKVLVRDLAARNLIVSLEDLYAVKSFGLAKAERKGDLSSRLPVKWTAPEALKHGF	401	QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
Db	300 YLESKVLVRDLAARNLIVSLEDLYAVKSFGLAKAERKGDLSSRLPVKWTAPEALKHGF	359	Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
RESULT 5			QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
ID	P77223 PRELIMINARY; PRT; 465 AA.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
AC	01-FEB-1997 (TREMBrel. 02, Created)		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DE	HYL tyrosine kinase.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
GN	MATK OR HYLTK.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
OS	Mus musculus (Mouse).		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
RN	[1]		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
RP	SEQUENCE FROM N.A.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
RC	STRAIN=CBX C57BL/6; TISSUE=Embryonic stem;		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
RX	MEDLINE=96280730; Pubmed=8644808;		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
RA	Hamaoguchi I., Yamaguchi N., Suda J., Hirao A., Hashiyama M.,		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
RT	*Analysis of CSK homologous kinase (csk/HYL) in hematopoiesis by utilizing gene knockout mice.";		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
RT	RL Biochem. Biophys. Res. Commun. 224:177-179(1996).		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
CC	-1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	EMBL: X33972; CAAS8806.1; -.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	HSSP; P11362; IFGK.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	MGD: MGI-99259; Matk.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	InterPro; IPR00719; Prot_kinase.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	InterPro; IPR00980; SH2.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	InterPro; IPR01452; SH3.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	InterPro; IPR00125; Tyr_pk kinase.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	Pfam; PF00069; pk kinase; 1.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	Pfam; PF00017; SH2; 1.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	Pfam; PF00018; SH2; 1.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	PRINTS; PRO00109; TYRKINASE.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	PRODom; PD000001; PROT_kinase; 1.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	PRODom; PD000093; SH2; 1.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	SMART; SM00252; SH2; 1.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	SMART; SM00326; SH3; 1.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	SMART; SM00329; TYRK; 1.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	PROSITE; PS50001; SH2; 1.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	PROSITE; PS50002; SH3; 1.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	PROSITE; PS50012; SH2; 1.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	PROSITE; PS50018; SH3; 1.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	PROSITE; PRO00401; SH2DOMAIN.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	PRINTS; PRO00109; TYRKINASE.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	PRODom; PD000001; PROT_kinase; 1.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	PRODom; PD000093; SH2; 1.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	SMART; SM00252; SH2; 1.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	SMART; SM00326; SH3; 1.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	SMART; SM00219; TYRK; 1.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		Db	180 ELARAGWLNLQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	PROSITE; PS50001; SH2; 1.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	PROSITE; PS50002; SH3; 1.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	PROSITE; PS50018; SH3; 1.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	PROSITE; PRO00401; SH2DOMAIN.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	PRINTS; PRO00109; TYRKINASE.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	PRODom; PD000001; PROT_kinase; 1.		Db	180 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239
DR	PRODom; PD000093; SH2; 1.		QY	282 KMQHENLVRLIGVTHQGLYTVMERVKSNLNVNLTTRALRVALNTAOLQFLSLIVAEQE	341
DR	SMART; SM00252; SH2; 1.		Db	60 AAALRQREALSTDPEKLSLMPWFHGKRSQEAQOLQPEDGLFLVRESARHKGDYVLCVS	119
DR	SMART; SM00326; SH3; 1.		QY	162 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	221
DR	SMART; SM00219; TYRK; 1.		Db	120 FGROWTHYVLHRGHLTDEAVFCFCNIMDVHYSKGNLNFTRGRALYSTSQLQFALHVACME	179
DR	SEQUENCE 465 AA.		QY	222 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	281
DR	SEQUENCE 465 AA.; Score 82.9%; Best local Similarity 89.5%; Pred No 1.9e-17; Matches 417; Conservative 24; Mismatches 24; Indels 1; Gaps 1;		Db	180 ELARAGWLNLNQHILTGQIGEGERGAVI-QGEYLQOKVAKVKNIKCDVTAQAFDETAVMT	239

Db	187	KRTEILOSAIFAKESFQREGWAPIEYEFKEKLGKGEIGNVVKWMAKTTVAKKRIDS	246
Qy	268	VTAQAFQLEDETAVMTKMOHENYLRLGVITH-OCLYIVMEHVSKGNLVNLPLTRGRALVNT	326
Db	247	KTAQSLIAEASYMTLHQHNLYLVLAISFQGDSILLTEYCEKGVLVLELRTRGRAVITL	306
Qy	327	AOLLOESLHVAGCMEYLESKKLVHRLDAARNLTVSLEDVAKVSDFGLAKAERKGDSLRL	386
Db	307	EBQKGPAFDVCMGMRLEEKNIHLRDLARVNLLSDELQCKVSDPGLAKDVEBIALSGF	366
Qy	387	PVKWTAPAEALKIFSTKSDWSFGVLLWEVSYGRAPYKMSLKEVAEBAVEKGYMEPP	446
Db	367	PVKWTAPAEALKIFSTKSDWSFGVLLWEVSYGRAPYKMSLKEVAEBAVEKGYMEPP	426
Qy	447	ECPGPVPHVLMSSCWEAEPARRPFPKLAEKL	478
Db	427	EKCPPFVYQMLKWCWADPSRRPSFKQQLHNL	458
RESULT 11			
ID	091x65	PRELIMINARY; PRT; 509 AA.	
AC	091x65;		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Similar to lymphocyte-specific protein tyrosine kinase.		
GN	LCK.		
OS	MUS musculus (Mouse).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TAXID=10090;			
RN	[1]		
RP	SEQUENCE FROM N A.		
RC	TISSUE=Salivary gland;		
RA	Strausberg R.;		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC01474; AAH11474.1; -.		
DR	MGD; MGI:96756; Lck.		
DR	InterPro; IPR00719; Prot_kinase.		
DR	InterPro; IPR00980; SH2.		
DR	InterPro; IPR01452; SH3.		
DR	InterPro; IPR01245; Tyr_pk kinase.		
DR	Pfam; PF00669; Pkinase_1.		
DR	Pfam; PF00117; SH2_1.		
DR	PRINTS; PRO0401; SH2DOMAIN.		
DR	PRINTS; PRO0452; SH3DOMAIN.		
DR	PRINTS; PR0109; TYRKINASE.		
DR	PRODOM; PD000001; Prot_kinase; 1.		
DR	PRODOM; PD000093; SH2_1.		
DR	SMART; SM00252; SH2; 1.		
DR	SMART; SM00326; SH3; 1.		
DR	SMART; SM00219; TYRK; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS50001; SH2; 1.		
DR	PROSITE; PS50002; SH3; 1.		
KW	ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.		
SO	SEQUENCE 509 AA; 57942 MW; 3513102F49A7FD0B CRC64;		
Query Match	28.1%; Score 751.5; DB 11; Length 509;		
Best Local Similarity	38.3%; Pred. No. 1.8e-52;		
Matches	164; Conservative 84; Mismatches 155; Indels 25; Gaps 9;		
Qy	65 GLAFLAFRGKDVTILEACENKSYWKRVKHNTSGGBGLAAGLRLREALSADPKLSSLMPFH	124	
Qy	65 GLAFLAFRGKDVTILEACENKSYWKRVKHNTSGGBGLAAGLRLREALSADPKLSSLMPFH	124	
Db	78 GDGFGERGEQLRILE---QSGWKAQSLLTGQBFIPNFVAKANSPE----PWF	129	
Qy	125 GKISGQBAVQLOPPE--GLELVRRESRHPGYVLCV---SFGROWVHYRLHRD-G	176	
Qy	: :		
Qy	177 HLTIDEAVFFCNLMDAEHVYSKDKGAICTKIVPRKRGHTSAAEELARAGNLLNQLHT	236	
Db	190 GFYVISPRITEFGFLHDIVRHYNAASDGICTKLSRPCQ---TKQPKQPKWEDWEVPRETLK	246	
Db	237 IGAQTCGEGERGAVQCGEYLSG-KVAVKNIK-CDVTAQAFQLEDETAVMTKMOHENYLRLGV	294	
Qy	: :		
Db	247 IVERLUGAQQRGEVWMGQYNGHTKVAVKSLKGQCSMSPDAFLAEANMKQLOQHPLPVRLIAY	306	
Qy	295 ILHQGLIVYMBHVSKGNLVNLTRGRALVTAQOLQFSLIVAVGMEYLESKKLVHDLA	354	
Db	307 VTQEPYIYTTPMGSVLSLVDIKTPPGKLNKLADMAIAEGMAFESQNYIHRD	366	
Qy	355 ARNLIVSEDLVAKVSDFGLAKA---ERKGIDSSRLPVKWTAPAEALKHGKFTSKDSWFS	410	
Db	367 ANILVSDTLCISKIADFGLARLIEDNEYTAREGAKFPIKWPRAPEAINYGTFTKDSWFS	426	
Qy	411 CYLLWIVFSTGRAPYKMSLFEVSEAVEKGYRMEPPFGCOPGVHLMSSCNEAEPARRP	470	
Db	427 GILLTLELVTHGRIPYPMGNTDEVIONLERGYRMVRPDNCPELYHMLMCWKERPEDRPT	486	
Qy	471 FRKLAKELI	478	
Db	487 FDYLRSYLT	494	
RESULT 12			
ID	09300	PRELIMINARY; PRT; 526 AA.	
AC	093080		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DE	TSU1 SRC (Fragment).		
GN	SRC.		
OS	Rous sarcoma virus.		
OC	Viruses; Retrovirus; Retroviridae; Alpharetrovirus.		
OX	NCBI-Taxid=11886;		
RN	[1]		
RP	SEQUENCE FROM N A.		
RX	MEDLINE=92278773; PubMed=1375718;		
RA	Maroney A.C., Qureshi S.A., Foster D.A., Brugge J.S.; RT "Cloning and characterization of a thermostable v-src gene for use in reversible transformation of mammalian cells.";		
RT	RT Oncogene 7:1207-1214(1992).		
CC	-- SIMILARITY: CONTAINS 1 SH3 DOMAIN.		
DR	EMBL; S37068; AAB96645.1; -.		
DR	HSSP; P00524; ISPR.		
DR	InterPro; IPR00719; Prot_kinase.		
DR	InterPro; IPR00980; SH2.		
DR	InterPro; IPR01452; SH3.		
DR	InterPro; IPR01245; Tyr_pk kinase.		
DR	Pfam; PF0069; kinase; 1.		
DR	Pfam; PF0017; SH2; 1.		
DR	Pfam; PF00018; SH3; 1.		
DR	PRINTS; PRO0401; SH2DOMAIN.		
DR	PRINTS; PRO0452; SH2DOMAIN.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	PRODOM; PD00001; Prot_kinase; 1..		
DR	PRODOM; PD00003; SH2; 1.		
DR	PRODOM; PD00066; SH3; 1.		
DR	SMART; SM00252; SH2; 1.		
DR	SMART; SM00326; SH3; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00019; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS50002; SH3; 1.		
KW	ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.		
SO	SEQUENCE 526 AA; 58970 MW; 22986AA2F3D1538 CRC64;		

Query Match		Score	DB	Length	Y
Best Local Similarity	Conservative	39.6%	Pred.	No. 1e-51;	
Matches	170;	Conervative	76;	Mismatches	15;
Indels	27;	Gaps	10;		
66	ELAFRKGVVTLFACENKSWYRKHHGSGQEGULAAAGALRERALSADPKLSSLMPWPHG	125	DR	SMART; SM00252; SH2; 1.	
99	DLSFKKGRLQLQVNTEC-NWWLAHSVTGQTGYIPSNTVAPSDSLQAE-----EWFG	151	DR	SMRT; SM00326; SH3; 1.	
126	KISQEAVQQLQPED-GLFLYRESARHPGDYVLCS---FGRDVHYRVLRD-GH	177	DR	PROSTE; PS00107; PROTEIN_KINASE_ATP; 1.	
152	KTRRSRRLNPNPGTFLRESETKGATCCLSPDFNAKGLNKHVKIRKLDSCG	211	DR	PROSTE; PS50011; PROTEIN_KINASE_TVR; 1.	
178	LTDDEAVFCNLMDMVEIYSKDKGAICTPL-YPKRKIGTKSAEEELARAGWLNLQH	235	DR	PROSTE; PS50001; SH2; 1.	
212	FVTSRQPFSSLQQLNAYSKHDGCLCHRLLNQPTSKRQTOG---JAKDAWEIPRESL	267	DR	PROSTE; PS50002; SH3; 1.	
236	TLGQAQIGGEFGAVLQGYLGL-QKVAVNIK-CDTVAFLDEFETAVMTKMQHENLYRIG	293	DR	PROSTE; PS50010; PROTEIN_KINASE_CD; 1.	
268	RLEVKGCGCFKGKVMGMGTWNGTTRAVKTKLPGTMSPAEFLQEAQVMKKLQHEKLVQYA	327	DR	PROSTE; PS50002; SH3; 1.	
294	VILHQGLYIVMEAVSKGVLNVFLTRGRALVNTAQOLQESLHLAEGMVELESKKLVHDL	353	Db	45 HSPQQLS---PSSPLFDNVLVAlSYEPKHKDGLFEKGDKLUISK-EDPEWLAESLT	100
328	WVSKEPTEVIVEMSKSGSLNIFKGEMKYLRLPQVLMQAQIASGMAVVERMYVHDL	387	Db	94 SGOEGLIAAGALLERELASDPKLSLMPWHEKGKISGEAVQOLQPP-EDGFLVRESAR	151
354	AARNILVVEDLVAKVSDGLAKA---ERKGDSLRPKWTAAEALKIGKFWKSDWS	409	Db	101 TQRQGTVPYNEV---AMST---MEIPEWFFKNISNEANRLLAPGNTQGSFLIRESET	153
388	RAANILVQENLVKVAKDGLARLIEDNEYTARGAKFPLKWTAAEALVYGRFTKSDWS	447	Db	152 HPGDVYLCV---SIGRDVHYRVLRHD-GHITIDEAVFCNLMDMVEHSSKDKGACT	205
410	FGVLLWEFSYGRAPPMSLKEVSEAEKGYMEPPGCPGPVHMLASSWCAEPARRP	469	Db	154 TPGSYSLSIRIDDSNYGDEVKHYRIRNMNDGGFYITAKISFNALKELVHOYHSRDSGICL	213
448	FGILLTELMTKGRVVPYPMGNGEVLDYERYGRMPCPPCPESLHDLMCOCWRDPERP	507	Db	206 KCR-DVYQAFLDEFETAVMTKMQHENLYRIGVILHQGLYIVMHRVSKVNLVNTTRGRAL	323
470	PFKLAELK	478	Db	214 KLVKPCO---SKAPQPKWQWDWEWEIPRESLKLERKLGAGQFCEWMAGIHNNERRVAKCL	270
508	TFEVYQAOQI	516	Db	265 KC-DVYQAFLDEFETAVMTKMQHENLYRIGVILHQGLYIVMHRVSKVNLVNTTRGRAL	323
RESULT	13		Db	306 KIGTMSVEAFLAENAMKSLQHMLHVLFAVTWTQEPFIVITVYEMENSLVDLYKTGSS	330
080GJ9	PRELIMINARY;	PRT;	Db	324 VNTAQIQLFSHVAEENEYLISKVYHDLAARNLIVSEDIVAKVSDGLAKA---ERK	379
080GJ9;			Db	331 LSINTLIDMASQARHGMATERNYIHDRLRANTLYVSHELICKIADFGLARIENNEYT	390
01-JUN-2002	(TREMBrel. 21, Created)		Db	380 GLDSSRLPKVWTAPEALKHGKFTSKSDWSFGVLLWEVFSGRAPPKMSLKEVSEAEVK	439
01-MAR-2003	(TREMBrel. 23, Last sequence update)		Db	391 AREGAREPKIPTAPEAINYGFSIKSDWWSFCGILTEIVTYGRIPPGMSNPIVEHOLEQ	450
SEQUENCE FROM N.A.			Db	440 GYMRERPEPGCPEGVHMLSSWEEAEPARRPFPKRKAKL	478
BRENNER S., VENKATESH B., YAP W.-H., CHOU C.-F., TAY A.W.N.,			Db	451 NYRMPKPENCDFGFLNFMLLCWRKEKDRPFDYLSVL	489
MEDLINE=21874085; PubMed=11867707;			RESULT	14	
ACM	095M32	PRELIMINARY;	ID	095M32	
DT	01-DEC-2001	(TREMBrel. 19, Created)	AC	095M32	
DT	01-DEC-2001	(TREMBrel. 19, Last sequence update)	DT	095M32	
DT	01-MAR-2003	(TREMBrel. 23, Last annotation update)	DT	095M32	
DE		LCK protein.	DE	095M32	
GN		LCK.	GN	095M32	
OS		Hylobates sp. (gibbon).	OS	095M32	
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.	OC	095M32	
NCBI TaxID=9581		[1]	NCBI TaxID=9581	095M32	
RN		SEQUENCE FROM N.A.	RN	095M32	
RP			RP	095M32	
RA			RA	095M32	
Picard C.;					
RL Thesis (2001); Department of Experimental Oncology laboratory, U.					
CC					
DR EMBL; AJ30182; CAC4027_1; -					
DR InterPro; IPR000719; Prot_kinase.					
DR InterPro; IPR000580; SH2.					
DR InterPro; IPR001452; SH3.					
DR InterPro; IPR001452; SH3.					
DR InterPro; IPR001452; Tyr_pk kinase.					
DR Pfam; PF00069; Phinase; 1.					
DR Pfam; PF00018; SH2; 1.					
DR ProDom; PD000001; Prot_kinase; 1.					
DR ProDom; PD000093; SH2; 1.					
DR ProDom; PD000066; SH3; 1.					
DR Pfam; PF00017; SH2; 1.					

PFam; PRO0018; SH3; 1.
DR PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
PRINTS; PRO0109; TYRKINASE.
PRODom; PD000001; PROT_kinase; 1.
PRODom; PD000093; SH2; 1.
PRODom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50017; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50019; PROTEIN_KINASE_TIR; 1.
DR PROSITE; PS50001; SH2; 1.
DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
SEQUENCE 509 AA: 57946 MW: FIBREFC237C8DBE CRC64;
SQ

Query Match 27.6%; Score 737.5; DB 6; Length 509;
Best Local Similarity 37.4%;保守性 87; Mismatches 156; Indels 25; Gaps 9;
Matches 160; Conservative 87; Mismatches 156; Indels 25; Gaps 9;

QY 65 GELAFPRKGVDVTLTILEACENSKWYRKRHTSGQEGGLIAAGALRERALSADPKLSLMPWFH 124
Db 78 GDGFEEFKGEORLIE-QSEWWKQSLTGQEGETIPFNNIVAKANSLPE-----PWFF 129
QY 125 GKISQEQAEAVQOLQPED-GFLFVYRESARHPGDVLYCV-----SGRDVHYRVLHRD-G 176
Db 130 KNLSRKDAEROLLAPGNTGSFLIRESESTAGSFSLSVRDQDONGEVVVKHYKIRNLNG 189
QY 177 HLTDDEAVFCNLMDDMVEHYSKDKGAIICLKVRPKHGKTSAAEBELARAGWLMLQHLT 236
Db 190 GFYVSPRITPPGLHLILVRYTNASQGLCTRSLRPOQ---TQKPOKPWEDEWVRETLK 246
QY 237 LGAQTGEGERGAVLQGEGYLQG-KVAVKNIK-CDVYQAOFDLETAATMKHQNENLRLLGV 294
Db 247 LVERLIGAGQGEVWMMGYIYNGHTKAVKSLSKQGSMSPDAFLAEANJMKOHQHRLRLYAV 306
QY 295 ILHQCQYTMEHVSKGNLYNFRTRGRALVNTAQQLQFSLHVAEQMEYLESKKLHVHDLA 354
Db 307 VTQEPIVITYEMENGSLVDFLKAPSGIKLTINKLIDMAQIAEGMAFERNYIHDRLL 366
QY 355 ARNIVLVEDLVLAKVSDFGLAKA---ERKGLDSSILPVKVTAAPEALKHGFTSKSDVWSF 410
Db 367 AANTIVSPTUSCKTADFLARLIELDEYAREGAKFPIKMTAPEINYGFTIKSDVWSF 426
QY 411 GVLMKEVFSYGRAPYKPKMSLKEVRSVAKEVGKYMELPECGPGVPHVIMSSWAEARRP 470
Db 427 GILFELEVTHGRIKPPGMNTPEVIONLNERFIRMVFDNPCEELKQMLMQLWERBDRPT 486
QY 471 FRKLAELK 478
Db 487 FDYLRSVL 494
RESULT 15
808362 ID Q86362 PRELIMINARY; PRT; 545 AA.
AC Q86362; DT 01-NOV-1996 (Tremblel. 01' Created)
DT 01-NOV-1996 (Tremblel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblel. 23, Last annotation update)
DE Pp62v.
DE SROM.
OS Rous sarcoma virus.
OC Viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID:11886;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96183936; PubMed=8607264;
RX Tatsosyan A., Yatsula B., Shtrutman M., Moinova E., Kaverina I.,
RA Musatina E., Leskov K., Mizenina O., Zueva E., Galothe G.,
RA Dezele P.;

RT "Two new isoforms of v-Src oncogene isolated from low and high
metastatic RSV-transformed hamster cells.";
RT Virology 216:347-355 (1996);
RL !- SIMILARITY: CONAINS 1 SH3 DOMAIN.
CC EMBL: X84074; CAA5881.1; .
DR HSSP: P00524; ISPR.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; pkines; 1.
DR Pfam; PF00177; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Prints; PR00452; SH2DOMAIN.
DR Prints; PR00109; TYRKINASE.
DR PRODom; PD000001; PROT_kinase; 1.
DR PRODom; PD000093; SH2; 1.
DR PRODom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50017; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50019; PROTEIN_KINASE_TIR; 1.
DR PROSITE; PS50001; SH2; 1.
DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
SEQUENCE 545 AA: 61037 MW: 4C4E3BC75266913 CRC64;
SQ

Query Match 27.6%; Score 736; DB 15; Length 545;
Best Local Similarity 35.6%;保守性 82; Mismatches 181; Indels 76; Gaps 16;
Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16;

QY 14 HQCDSSAELPRL-----VSPIFLRWHPP-----PVSARMPTRWAPGTR----- 51
Db 26 HGGFPASQTPNPKTAPLTAAPRSSR-RPPASOHRRAAPDTHTPSSRF-GTVANEKPLF 81
QY 52 -----OCITKCEHTRPKPG-----ELAKRGVDVUTILEACENSWYR 88
Db 82 GDFNTSDTPTSPORARTFLAGVITFVALYDYESWIEIDLSFKKGERLQIVNNTEG-NWWL 140
QY 89 VVHHTSQEGGLIAAGALRERERALSADPKLSLMPWFHKGKISGQEAQVQOLQPED-GFLV 146
Db 141 AHSVTGTQTYIPSNTVAPSQIKA-----EWYCKITRREGSRGLINPBPGLVY 194
QY 147 RESARHPGDYVIVCS----FGRDVTYRVLHRD-GHILTDEAVFCNLMDDMVEHYSKDK 200
Db 195 RESETTKGAYCLSVSDEDNAKGLNWKHYKIRKDGGFYIISRTQFSSLQQLVAYISKHA 254
QY 201 GAICTKL-VPRPKHCTSKAEEELARAGWLNLQHLTIGQIGESEFGAVIQLQEVLYG-Q 257
Db 255 DGICHLRHTNVCPSTSPOTOG---LAKDAWEIIPRESLRLEVKGQGCFGEVNGTWNGTT 310
QY 258 KVAVKNIK-CDVYQAFLDETAATMKHQNENLRLGQVILHGLYIYMEHVSKGNLYNFL 316
Db 311 RYAIKTLKPGTMSPEAFQLQEVYQMKLKRHEKJYVOLYAVSERPIVIVYEVSKGLNL 370
QY 317 RYRGRALVNTAQALLOFLHVAEQMEYLFESKLVYVHDLAARNITLVEDLVLAVSKDFGLAKA 376
Db 371 KGEMGVKLRLPOLVDMQAQISGMAYERMVNHVRDIAANLNGELECKVADFGLARL 430
QY 377 ---ERKGLDSSRLPVKWTAAPEALKHGFTSKDWSFGVULIMEVFSYGRAPYKMSLKE 432
Db 431 TIEDNEYTARQGKPAKWTAAPEAGLYGFTKTSWDNSFGILLTETKGRGPYPGMNGE 490
QY 433 VSEAIVEKGYMRPEPEGCPGPVIVLMSSCWEAEPARRDPFRKLAELK 478
Db 491 VLDVRVERGYRPMCPPECPESTHDLMCOCCRREPEERPTFEVQAO 536

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